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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 23.62 Seconds
(without alignments)
348.101 million cell updates/sec

Title: US-09-978-189-370
Perfect score: 587
Sequence: 1 MSLLPRAPVSMRLAAL.....TKRFLKWNANNEKRYVEE 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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19: /SID58/gcgdata/geneseq/geneseqp/AA1998.DAT.*
20: /SID58/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SID58/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /SID58/gcgdata/geneseq/geneseqp/AA2001.DAT.*
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	587	100.0	111	20	AAV41739	Human PRO273 protein.
2	587	100.0	111	20	AAV28290	Tim-1 protein. Homo
3	587	100.0	111	21	AAH44295	Human PRO273 (UNC)
4	587	100.0	111	21	AAH34323	Human PRO273 protein
5	587	100.0	111	22	AAH88478	Human membrane or
6	582	99.1	111	18	AAW29291	Human chemokine a
7	527	89.8	99	20	AAV31612	Human neokine-1.
8	522	88.9	99	18	AAW29292	Human chemokine a
9	509	86.7	95	21	AAV76089	Human CXc chemokine
10	509	86.7	95	22	AAH5871	Human CXc chemokine
11	509	86.7	95	22	AAH56028	Human cell protein.

12	506	86.2	99	20	AAV31613
13	506	86.2	99	21	AAV76085
14	506	86.2	99	21	AAV76115
15	506	86.2	99	22	AAV56024
16	506	86.2	99	22	AAV56054
17	506	86.2	99	22	AAV56075
18	505	86.0	94	20	AAV31615
19	481	81.9	91	19	AAV69991
20	446	76.0	102	19	AAV69991
21	431	73.4	78	20	AAV31614
22	428	72.9	77	21	AAV76091
23	428	72.9	77	22	AAV56030
24	424	72.2	77	21	AAV76090
25	424	72.2	77	22	AAE05370
26	424	72.2	77	22	AAV56029
27	383.5	65.3	202	21	AAV56342
28	327	55.7	123	19	AAV66992
29	298	50.8	133	21	AAV75979
30	298	50.8	133	22	AAV55918
31	208	35.4	44	22	AAV32558
32	143.5	24.4	100	17	AAV90928
33	138	23.5	100	11	AAV05790
34	138	23.5	100	13	AAV20588
35	138	23.5	100	13	AAV20528
36	128.5	21.9	102	16	AAV70793
37	128.5	21.9	107	13	AAV20589
38	128.5	21.9	107	13	AAV20529
39	128.5	21.9	107	13	AAV20304
40	128.5	21.9	107	20	AAV96614
41	128.5	21.9	107	21	AAV15810
42	128.5	21.9	131	22	AAV25812
43	117.5	20.0	107	16	AAV70792
44	117.5	20.0	107	20	AAV96713
45	117.5	20.0	107	21	AAV15793

ALIGNMENTS

RESULT	1
AA41739	
ID	AA41739 standard; Protein; 111 AA.
XX	
AC	AA41739;
XX	
DT	07-DEC-1999 (first entry)
XX	
DE	Human PRO273 protein sequence.
XX	
KW	Human; PKO; EST; expressed sequence tag; PCR primer; hybridisation;
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder
KW	secreted protein; transmembrane protein.
XX	
OS	Homo sapiens.
XX	
PN	WO946281-A2.
XX	
PD	16-SEP-1999.
XX	
PE	08-MAR-1999; 99WO-US05028.
XX	
PR	10-MAR-1998; 98US-0077450.
PR	11-MAR-1998; 98US-0077632.
PR	11-MAR-1998; 98US-0077641.
PR	11-MAR-1998; 98US-0077649.
PR	12-MAR-1998; 98US-0077791.
PR	13-MAR-1998; 98US-0078004.
PR	17-MAR-1998; 98US-0040220.
PR	20-MAR-1998; 98US-0078886.
PR	20-MAR-1998; 98US-0078910.
PR	20-MAR-1998; 98US-0078936.
PR	20-MAR-1998; 98US-0078939.
PR	25-MAR-1998; 98US-0079294.

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PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079669.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080185.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 26-APR-1998; 98US-0083336.
PR 26-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085589.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086410.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.

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PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX
PA (GENE) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR N-PSDB; AA234205.
XX
DR WPI: 1999-551358/46.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
XX
PS Claim 12; Fig 149; 530pp; English.
XX
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA23391 to
CC AA24338, and AA241685 to AA241774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 111 AA;
XX
XX
Query Match 100.0%; Score 587; DB 20; Length 111;
Best Local Similarity 100.0%; Pred. No. 2,3e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLLPRAPPVSMRLAALLLLALTYARVDGSKCKSCRKGPRIKRSVKKLEMKRY 60
DB 1 msllprappvsrmllaaalllllalyarvdgskckscrkpkrlysdvkklempky 60
QY 61 PHEEKWVILITKSVSRGSGECLHPKIOSTRFKTKWNAWEKRYEE 111
DB 61 pheeekwvilitksvsrsgsgelhpkiqstkrfkikwnawekrryee 111
DB
RESULT 2
AA28290
ID AAY28290 standard; Protein; 111 AA.
XX
AC AAY28290;
XX
DT 28-SEP-1999 (first entry)
XX
DE Tim-1 protein.
XX
XX Chemokine; CXCL1; inflammation; heart attack; stroke; infection; ss;
XX trauma; radiation; burns; frostbite; corrosive chemical; gene therapy.
XX
OS Homo sapiens.
XX
XX WO9333990-A1.
XX
PD 08-JUL-1999.
XX
PF 14-DEC-1998; 98WO-US26546.
XX
PR 30-DEC-1997; 97US-0068955.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Chen TT, Kassam A, Pot D;
XX
XX WPI: 1999-430244/36.

```

DR N-PSDB; AAX89708.
 XX
 PT A new human CXG chemokine, Tim-1, useful for treating inflammation
 XX
 PS Claim 1; Page 43; 46pp; English.
 CC
 CC This is the amino acid sequence for the Tim-1 CXG chemokine. The Tim-1
 CC gene can be used to design therapeutic tools for treating inflammation
 CC due to stimuli such as heart attacks and stroke, infection, physical
 CC trauma, UV or ionizing radiation, burns, frostbite or corrosive
 CC chemicals. The Tim-1 gene and subgenomic polynucleotides can be used
 CC in gene therapy.
 CC
 SO Sequence 111 AA:
 Query Match 100.0%; Score 587; DB 20; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.3e-60;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLLPRAPVSMRLAALLLLALYARVDGSKCCKSRGPKIRYSDVKLEMKPKY 60
 DB 1 msllprapvsmrllaaalllllalytarvdgskckcsrkpgkrlrdsdkklemkpxy 60
 QY 61 PHEEKWVITTTKSVSRGGEHCLHPKLOSTRKRTKRYNMNKKRYVEE 111
 DB 61 pheeekwvittkksvstrygechlpklostrkrtkrynmnkkryvee 111
 RESULT 3
 ID AAB44295 standard; Protein: 111 AA.
 AC AAB44295;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO273 (UNQ240) protein sequence SEQ ID NO:370.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
 KW expressed sequence tag; detection; cancer.
 OS Homo sapiens.
 XX
 OS MO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kiljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart RA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI: 2000-611443/58.
 DR N-PSDB; AAC78551.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 PS Claim 12; Fig 149; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells; AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 CC
 SQ Sequence 111 AA:
 Query Match 100.0%; Score 587; DB 21; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.3e-60;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLLPRAPVSMRLAALLLLALYARVDGSKCCKSRGPKIRYSDVKLEMKPKY 60
 DB 1 msllprapvsmrllaaalllllalytarvdgskckcsrkpgkrlrdsdkklemkpxy 60
 QY 61 PHEEKWVITTTKSVSRGGEHCLHPKLOSTRKRTKRYNMNKKRYVEE 111
 DB 61 pheeekwvittkksvstrygechlpklostrkrtkrynmnkkryvee 111
 RESULT 4
 ID AAB33423 standard; Protein: 111 AA.
 AC AAB33423;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO273 protein UNQ240 SEQ ID NO:46.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 KW antianemic; hepatotropic; vitruic; antiprolitic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 OS Homo sapiens.
 XX
 OS MO200053758-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99US-0123618.
 PR 12-MAR-1999; 99US-0123957.
 PR 23-MAR-1999; 99US-0125775.
 PR 12-APR-1999; 99US-0128849.
 PR 20-APR-1999; 99WO-US08615.
 PR 28-APR-1999; 99US-0133445.
 PR 04-MAY-1999; 99US-0133771.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tamas D, Watanabe CK, Wood WT, Yan M;
 XX
 DR N-PSDB; AAC58588.
 XX
 WI: 2000-572271/53.
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX
 XX
 PS Claim 33; Fig 20; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC5397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 587; DB 21; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2, 3e-60;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLLPRRAPVSMRLAALLLLALTYARVDSKCKSKGKIRYSDVKIKLEMPKY 60
 Db 1 msllprapvsmrllaaallllaltyarvdsckskckskgkirkysdvkiklemkpy 60
 QY 61 PHCEEKWVITTTKSYRSGEHCLEPLOS TKRFRKMYNMMNKKRYVEE 111
 Db 61 phceekwvlttksvrsgehclpqlsgskfrkmywnmknkryvee 111
 Db
 RESULT 5
 AAB88478
 ID AAB88478 standard; Protein: 111 AA.
 XX
 AC AAB88478;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Human membrane or secretory protein clone PSEC0212.
 XX
 KM Human; secretory protein; membrane protein; vaccine; gene therapy;
 KM rheumatoid arthritis; diabetes.
 OS Homo sapiens.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114090.
 XX
 PR 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX
 PA (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 PI WPI: 2001-093989/71.
 DR N-PSDB; AAF93905.
 XX
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -
 XX
 XX
 PS Claim 1; SEQ ID 324; 609pp + CD ROM; English.
 XX
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to

CC identify modulators (agonists and antagonists) of expression and
 CC activity. The antibodies and antagonists may also be used as therapeutic
 CC agents to down regulate expression and activity. The antibodies may also
 CC be used as diagnostic agents for detecting the presence of the
 CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay
 CC (ELISA). Examples of diseases which may be treated include rheumatoid
 CC arthritis and diabetes.

XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 587; DB 22; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.3e-60;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLPRRAPVSMRLAALLLLALLATYARVDSKCKSRKGRKIRYSDVKLEMPKY 60
 Db 1 msllprappvsmrllaaalllllallatarydsgskcksrkgrkirydvkklmky 60
 QY 61 PHEEKWVITTKSVSRVSGOEHCLHPKLOSTKRPIKWTNANNEKRRVYEE 111
 Db 61 phceekwvittksvsrvsgoehclhpklostkrpikwtanannekrrvyee 111

RESULT 6

AAW29291
 ID AAW29291 standard; Protein; 111 AA.

XX
 AC AAW29291;

DT 14-APR-1998 (first entry)

XX
 DE Human chemokine alpha-2.

XX
 KW Human chemokine alpha-2; Ckalpha-2; treatment; prevention; tumour;
 KW leukaemia; T-cell mediated autoimmune disease; parasitic infection;
 KW psoriasis; asthma; allergy; haematopoiesis regulation;
 KW growth factor stimulation; angiogenesis inhibition;
 KW wound healing promotion; antagonist; rheumatoid arthritis;
 KW autoimmune disease; inflammatory disease; infective disease;
 KW allergic reaction; prostaglandin-independent fever;
 KW bone marrow failure.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..28
 FT /label= sig_peptide

FT Peptide 29..111
 FT /label= mat_peptide

XX
 PN WO9735010-A1.

XX
 PD 25-SEP-1997.

XX
 PF 19-MAR-1997; 97WO-US04329.

XX
 PR 19-MAR-1996; 96US-0013653.

XX
 PA (HUMA-) HUMAN GENOME SCI INC.

XX
 PI Gentz RL, Li H, Ni J, Su JY;

XX
 DR WPI: 1997-480216/44.

XX
 DR N-PSDB; AAT86316.

XX
 PT Novel human chemokine alpha 2 and DNA encoding it - useful for
 PT treatment of leukaemia, tumours, autoimmune disease, wound healing,
 PT psoriasis, chronic infections and fibrotic disorders

XX
 PS Claim 14; Pages 66-67; 82pp; English.

XX
 CC The present sequence is human chemokine alpha-2 (Ckalpha-2),

CC which can be used to treat and/or prevent tumours, leukaemia,
 CC T-cell mediated autoimmune diseases, parasitic infections,
 CC psoriasis, asthma and allergy; regulate haematopoiesis, stimulate
 CC growth factor activity; inhibit angiogenesis and promote wound
 CC healing. Ckalpha-2 antagonists can be used to treat rheumatoid
 CC arthritis, autoimmune and chronic and acute inflammatory and
 CC infective diseases, allergic reactions, prostaglandin-independent
 CC fever and bone marrow failure.

XX
 SQ Sequence 111 AA;

Query Match 99.1%; Score 582; DB 18; Length 111;
 Best Local Similarity 99.1%; Pred. No. 8.6e-60;
 Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSLLPRRAPVSMRLAALLLLALLATYARVDSKCKSRKGRKIRYSDVKLEMPKY 60
 Db 1 msllprappvsmrllaaalllllallatarydsgskcksrkgrkirydvkklmky 60
 QY 61 PHEEKWVITTKSVSRVSGOEHCLHPKLOSTKRPIKWTNANNEKRRVYEE 111
 Db 61 phceekwvittksvsrvsgoehclhpklostkrpikwtanannekrrvyee 111

RESULT 7

AAV31612
 ID AAV31612 standard; Protein; 99 AA.

XX
 AC AAV31612;

DT 20-OCT-1999 (first entry)

XX
 DE Human neokine-1.

XX
 KW Chemottractant cytokine; chemokine; CXG motif; conserved cysteine;
 KW signal transduction modulation; angiogenesis inhibition;
 KW chemotraction inhibition; cancer; inflammation; psoriasis;
 KW post-transplantation organ rejection.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= signal_peptide

FT Protein 23..99
 FT /note= "Human mature neokine-1"
 FT Region 25..72
 FT /label= CXG_motif
 FT /note= "Conserved Cys at 25, 27, 51 and 72"

XX
 PN WO9940104-A1.

XX
 PD 12-AUG-1999.

XX
 PF 10-FEB-1999; 99WO-US02943.

XX
 PR 10-FEB-1998; 98US-0023664.

XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX
 PI Barnes TM, Mackay C;

XX
 DR WPI: 1999-494271/41.

XX
 DR N-PSDB; AA208962.

XX
 PT Novel neokine polypeptides and polynucleotides used for regulating
 PT and treating proliferative disorders and diseases

XX
 PS Disclosure; Fig 1; 123pp; English.

XX
 CC This sequence represents human neokine-1. Human expressed
 CC sequence tags (ESTs), potentially encoding a chemokine, were

PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
 PI WPI: 2000-072177/06.
 DR N-PSDB; AAB61797.
 XX
 PT Novel polynucleotides useful for the treatment of various conditions
 XX including wounds and cancer -
 PS
 PS Claim 4: Page 202; 235pp: English.
 XX
 CC The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transil amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
 CC by cDNA sequences derived from several mouse, rat or human skin cell
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
 CC putative transmembrane domains.
 XX
 SO Sequence 95 AA:
 XX
 Query Match 86.7%; Score 509; DB 21; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2e-51;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 AAILLLLLALYTAARDGSKCKSRKPKIRYSDVKLEMKPKYPHCEKMWIITTKSVS 76
 Db 1 aaaillllllalytarvsgskcksrkpkirysdvkklmkpkypheekmwilttksvs 60
 QY 77 RYRGDECHLPKLOSTKRFIKWYNANNEKRYVEE 111
 Db 61 ryrgechlpkqlgstkrfifkynawnekrvyee 95
 RESULT 10
 AAE05371
 ID AAE05371 standard; Protein; 95 AA.
 XX
 AC AAE05371;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Human hUKS1 protein.
 XX
 KW Human; cytostatic; antiinflammatory; immunoregulatory; tissue integrity;
 KW wound healing; immune response; vaccine; cancer; asthma; allergy;
 KW cell trafficking; therapy; hUKS1.
 XX
 OS Homo sapiens.
 XX
 PN WO200148192-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 21-DEC-2000; 2000WO-NZ00256.
 XX
 PR 23-DEC-1999; 99US-0171678.
 PR 28-NOV-2000; 2000US-0724864.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX

PI Watson JD, Murison JG;
 XX
 DR WPI: 2001-425665/45.
 DR N-PSDB; AAD10141.
 XX
 PT Novel isolated polypeptide useful to isolate corresponding interacting
 XX proteins or other compounds, to quantitatively determine levels of
 PS interacting proteins or other compounds, and as therapeutic target -
 PS
 PS Example 2: Page 94; 101pp: English.
 XX
 CC The patent discloses novel polynucleotides and their corresponding
 CC proteins which play a major role in induction of growth, cell migration
 CC and proliferation, cell-cell interaction and the differentiation of
 CC tissue-specific cells. These proteins are important in the maintenance
 CC of tissue integrity and thus are important in wound healing. They are
 CC useful in various assays to determine the biological activity, to raise
 CC antibodies, to isolate corresponding interacting proteins or other
 CC compounds, to quantitatively determine levels of interacting proteins or
 CC other compounds, and as therapeutic target in a whole range of disease
 CC states. Compositions comprising the novel proteins of the invention are
 CC useful for treating mammalian disorders. Polynucleotides of the invention
 CC are useful in genome and physical mapping, in positional cloning of
 CC genes, to tag or identify an organism or its reproductive material (as
 CC non-disruptive tags for marking organisms), and for the diagnosis and
 CC treatment of mammalian diseases which is the consequence of inappropriate
 CC expression of kinase genes. They are useful for promoting immune response
 CC as part of a vaccine or anti-cancer treatment, as target for cancer
 CC treatment, as immunoregulatory and anti-inflammatory molecule, as
 CC diagnostic for specific types of cancer and for development of an
 CC anti-cancer treatment, and as a target for antagonists in the treatment
 CC of diseases such as asthma and allergy. They are also useful to inhibit
 CC or enhance the activity of the soluble molecule that binds proteins of
 CC the invention, for tissue and neural regeneration, to promote or block
 CC cell trafficking, and as anti-inflammatory and/or vaccine adjuvant.
 CC The present sequence is human hUKS1 protein.
 XX
 SO Sequence 95 AA:
 XX
 Query Match 86.7%; Score 509; DB 22; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2e-51;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 AAILLLLLALYTAARDGSKCKSRKPKIRYSDVKLEMKPKYPHCEKMWIITTKSVS 76
 Db 1 aaaillllllalytarvsgskcksrkpkirysdvkklmkpkypheekmwilttksvs 60
 QY 77 RYRGDECHLPKLOSTKRFIKWYNANNEKRYVEE 111
 Db 61 ryrgechlpkqlgstkrfifkynawnekrvyee 95
 RESULT 11
 AAB56028
 ID AAB56028 standard; Protein; 95 AA.
 XX
 AC AAB56028;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Skin cell protein, SEQ ID NO: 344.
 XX
 KW Human; skin cell; cytostatic; antiinflammatory; anti-HIV;
 KW neutrophic; neuroprotective; vulnerary; immunomodulatory; vaccine;
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
 KW inflammation; neurological disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200069884-A2.
 XX
 PD 23-NOV-2000.
 XX

XX 15-MAY-2000; 2000MO-N200075.
 PF
 XX 14-MAY-1999; 99US-0312283.
 PR
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA
 XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murlison JG;
 PI
 XX WPI; 2001-007495/01.
 DR
 XX N-PSDB; AAC9730.
 DR
 XX
 PT New isolated polynucleotide used in the identification of genetic
 PT disorders and encoding polypeptides used for treating inflammatory
 PT disease, cancer and neurological diseases -
 XX
 PS Claim 4; Page 270; 352pp; English.
 PS
 XX The present sequence is a polypeptide which is expressed in
 CC mammalian skin cells. The polypeptide is useful for stimulating
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
 CC tumours, modulating skin inflammation, stimulating the growth of
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
 CC neurological diseases. The polynucleotide can be used as a marker, in
 CC the identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns.
 CC
 SQ Sequence 95 AA:
 XX
 Query Match 86.7%; Score 509; DB 22; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2e-51;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 17 AALLLLALLLYTARVDGSKCKSRGPKIRISDVKKLEMKPKYPHCEKMWITTTKVS 76
 DB 1 aaalllllllalytarvdgskcksrkpkirysdvkklmkpkypheekmwilttkvs 60
 OY 77 RYRGQEHCHLPKIOSTKRFIKWYNANNEKRRVVEE 111
 DB 61 ryrqgqehchlpklsqstkrfkikwynamnekriryee 95
 Db
 RESULT 12
 AAY31613
 ID AAY31613 standard; Protein: 99 AA.
 XX
 AC AAY31613;
 XX
 DT 20-OCT-1999 (first entry)
 XX
 DE Murine neokine-1.
 XX
 XX Chemoattractant cytokine; chemokine; CXC motif; conserved cysteine;
 KW signal transduction modulation; angiogenesis inhibition;
 KW chemoattraction inhibition; cancer; inflammation; psoriasis;
 KW post-transplantation organ rejection.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= Signal_peptide
 FT Protein 23..99
 FT /note= "Murine mature neokine-1"
 FT Region 25..72
 FT /label= CXC_motif
 FT /note= "Conserved Cys at 25, 27, 51 and 72"
 XX
 XX WO9940104-A1.
 XX

PD 12-AUG-1999.
 XX
 PF 10-FEB-1999; 99WO-US02943.
 XX
 PR 10-FEB-1998; 98US-0023664.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Barnes TM, Mackay C;
 XX
 DR WPI; 1999-494271/41.
 DR N-PSDB; AA208963.
 XX
 PT Novel neokine polypeptides and polynucleotides used for regulating
 PT and treating proliferative disorders and diseases
 XX
 PS Claim 1; Fig 2; 123pp; English.
 PS
 XX This sequence represents murine neokine-1. The neokines are a novel
 CC family of chemoattractant cytokines (chemokines) and are ligands for a
 CC previously identified putative G protein-coupled receptor termed RDC1
 CC (also called the neokine receptor). The neokines are members of the
 CC non-ELR-CXC subfamily of chemokines characterised by the absence of an
 CC ELR motif and the presence of a CXC signature motif. The CXC motif
 CC encompasses 4 highly conserved cysteine residues, with the first two
 CC cysteines separated by one non-conserved amino acid residue; however,
 CC the neokines show some atypical features which distinguish them from
 CC previously characterised CXC chemokines e.g., the presence of
 CC approximately 5 residues between the third and fourth conserved
 CC cysteines. The neokines have a variety of functions, including
 CC modulation of signal transduction, inhibition of angiogenesis,
 CC regulation of inflammation and inhibition of chemoattraction.
 CC Neokines may therefore be useful in the treatment of various
 CC proliferative disorders or diseases: several types of cancer,
 CC inflammation, psoriasis, and immune rejection following skin graft
 CC and kidney transplantation. Neokines, their associated polynucleotides,
 CC homologues and antibodies can be used in screening for drugs or
 CC compounds which modulate their activity and therefore may be important
 CC for the development of new therapeutics.
 CC
 SQ Sequence 99 AA:
 XX
 Query Match 86.2%; Score 506; DB 20; Length 99;
 Best Local Similarity 94.9%; Pred. No. 4.7e-51;
 Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 13 MRLAALLLLALLYTRVDGSKCKSRGPKIRISDVKKLEMKPKYPHCEKMWITTT 72
 DB 1 mrlaalllllllalcasrvdgsckcsrkpkirysdvkklmkpkypheekmwivlt 60
 OY 73 KVSRYRGQEHCHLPKIOSTKRFIKWYNANNEKRRVVEE 111
 DB 61 kmsriryqgqehchlpklsqstkrfkikwynamnekriryee 99
 Db
 RESULT 13
 AAY76085
 ID AAY76085 standard; Protein: 99 AA.
 XX
 AC AAY76085;
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE Murine CXC chemokine homologue muKSL, SEQ ID NO:340.
 XX
 XX Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery.
 KW
 XX


```

OS Mus sp.
XX WO9955865-A1.
XX
XX PD 04-NOV-1999.
XX
XX PF 29-APR-1999; 99WO-N200051.
XX
XX PR 29-APR-1998; 98US-0069726.
XX
XX PR 09-NOV-1998; 98US-0188930.
XX
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX PI Strachan L, Sleeman M, Watson JD, Orrust R, Kumble A, Morrison JG;
XX
XX DR WPI: 2000-072177/06.
XX
XX DR N-PSDB; AA261790.
XX
XX PT Novel polynucleotides useful for the treatment of various conditions
XX including wounds and cancer -
XX
XX PS Claim 4; Page 200; 235pp; English.
XX
XX CC The invention relates to novel nucleic acid sequences derived from rat
XX CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
XX CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
XX CC cells. Polypeptides of the invention may be used to treat inflammation,
XX CC cancer and neurological diseases. The proteins may be used to stimulate
XX CC the growth and motility of keratinocytes, to inhibit the growth of
XX CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
XX CC modulate skin inflammation, to modulate epithelial cell growth and to
XX CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
XX CC to treat growth and developmental defects, skin wounds and hair follicle
XX CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
XX CC by cDNA sequences derived from several mouse, rat or human skin cell
XX CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
XX CC AAY76119 are proteins with an N-terminal signal sequence, indicating
XX CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
XX CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
XX CC putative transmembrane domains.
XX
XX SQ Sequence 99 AA;
XX
XX
XX Query Match 86.2%; Score 506; DB 21; Length 99;
XX Best Local Similarity 94.9%; Pred. No. 4.7e-51;
XX Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX OY 13 MRLIAAALLLLALYTVARYDSKCKSRKGRKIRYSDVKLEMPKYPHCEKMTIT 72
XX ||||||||| :|||||||||
XX Db 1 mrliaaalllllalcasrvdsgkcksrkgrkirydsdkklemppkypheekmviytl 60
XX
XX OY 73 KSVSRVSGOEHCHPKLOSTKRIRIKYNNAMNEKRRYEE 111
XX ||:|||||||||
XX Db 61 kmsryrgchclhpklgsktkrikwynamnekriryee 99
XX
XX
XX RESULT 14
XX ID AAY76115
XX ID AAY76115 standard; Protein; 99 AA.
XX
XX AC AAY76115;
XX
XX DT 27-MAR-2000 (first entry)
XX
XX DE Full-length murine CXCL chemokine homologue muKSL, SEQ ID NO:394.
XX
XX SKIN; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
XX KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
XX KW secreted; transmembrane; inflammation; cancer; neurological disease;
XX KW angiogenesis; tumour vascularisation; growth disorder;
XX KW developmental disorder; skin wound; hair follicle disorder;
XX KW anti-inflammatory; cytostatic; neuroprotective; vulnery.

```

```

XX OS Mus sp.
XX WO9955865-A1.
XX
XX PN 04-NOV-1999.
XX
XX PD 29-APR-1999; 99WO-N200051.
XX
XX PF 29-APR-1998; 98US-0069726.
XX
XX PR 09-NOV-1998; 98US-0188930.
XX
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX PI Strachan L, Sleeman M, Watson JD, Orrust R, Kumble A, Morrison JG;
XX
XX DR WPI: 2000-072177/06.
XX
XX DR N-PSDB; AA261823.
XX
XX PT Novel polynucleotides useful for the treatment of various conditions
XX including wounds and cancer -
XX
XX PS Claim 4; Page 223; 235pp; English.
XX
XX CC The invention relates to novel nucleic acid sequences derived from rat
XX CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
XX CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
XX CC cells. Polypeptides of the invention may be used to treat inflammation,
XX CC cancer and neurological diseases. The proteins may be used to stimulate
XX CC the growth and motility of keratinocytes, to inhibit the growth of
XX CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
XX CC modulate skin inflammation, to modulate epithelial cell growth and to
XX CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
XX CC to treat growth and developmental defects, skin wounds and hair follicle
XX CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
XX CC by cDNA sequences derived from several mouse, rat or human skin cell
XX CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
XX CC AAY76119 are proteins with an N-terminal signal sequence, indicating
XX CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
XX CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
XX CC putative transmembrane domains.
XX
XX SQ Sequence 99 AA;
XX
XX
XX Query Match 86.2%; Score 506; DB 21; Length 99;
XX Best Local Similarity 94.9%; Pred. No. 4.7e-51;
XX Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX OY 13 MRLIAAALLLLALYTVARYDSKCKSRKGRKIRYSDVKLEMPKYPHCEKMTIT 72
XX ||||||||| :|||||||||
XX Db 1 mrliaaalllllalcasrvdsgkcksrkgrkirydsdkklemppkypheekmviytl 60
XX
XX OY 73 KSVSRVSGOEHCHPKLOSTKRIRIKYNNAMNEKRRYEE 111
XX ||:|||||||||
XX Db 61 kmsryrgchclhpklgsktkrikwynamnekriryee 99
XX
XX
XX RESULT 15
XX ID AAB56024
XX ID AAB56024 standard; Protein; 99 AA.
XX
XX AC AAB56024;
XX
XX DT 08-MAR-2001 (first entry)
XX
XX DE Skin cell protein, SEQ ID NO: 340.
XX
XX SKIN cell
XX KW Mouse; skin cell; cytostatic; anti-inflammatory; anti-HIV;
XX KW neurotrophic; neuroprotective; vulnery; immunomodulatory; vaccine;
XX KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
XX KW inflammation; neurological disease.

```

OS Mus sp.

XX WO200069884-A2.

XX 23-NOV-2000.

XX 15-MAY-2000; 2000WO-NZ00075.

XX 14-MAY-1999; 99US-0312283.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

XX WPI; 2001-007495/01.

XX N-PSDB; AAC99723.

XX New isolated polynucleotide used in the identification of genetic
XX disorders and encoding polypeptides used for treating inflammatory
XX disease, cancer and neurological diseases -

XX Claim 4; Page 268; 352pp; English.

CC The present sequence is a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in
CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.

XX Sequence 99 AA;

SQ Query Match 86.2%; Score 506; DB 22; Length 99;

Best Local Similarity 94.9%; Pred. No. 4.7e-51;

Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 13 MRLAAALLLLALATYARVDSKCKSRKGRIRYSDVKLEMKPKYPHCEKVIIT 72

Db 1 mlllaaallllllalcastrvdgskcksrkgrirysdvkkllemkpkypheekmivlt 60

QY 73 KSVSRIRGQEHCLHPKLOSTKRPRIKYNANNEKRYEE 111

Db 61 kmsrirygqehclhpklgstkrfkwyannekriryee 99

Search completed: January 29, 2002, 16:04:06
Job time: 32 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 12.49 Seconds

(without alignments)
199,989 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 587

Sequence: 1 MSLLPRRAPVSMRLAAAL.....TKRFIKYNAWNEKRYVEE 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*

4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*

5: /cgn2_6/prodata/2/1aa/PCRTUS.COMB.pep:*

6: /cgn2_6/prodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	99.1	111	2	US-08-825-556A-2
2	522	88.9	99	4	US-08-825-556A-3
3	509	86.7	95	4	US-09-188-930-344
4	506	86.2	99	4	US-09-188-930-340
5	428	72.9	77	4	US-09-188-930-346
6	424	72.2	77	4	US-09-188-930-345
7	298	50.8	133	4	US-09-188-930-157
8	143.5	24.4	98	2	US-08-825-556A-4
9	143.5	24.4	100	4	US-08-679-492A-146
10	138	23.5	100	3	US-08-476-376-2
11	128.5	21.9	107	1	US-08-352-324A-4
12	128.5	21.9	107	2	US-08-862-607-4
13	128.5	21.9	107	2	US-08-468-819-6
14	128.5	21.9	107	2	US-09-203-235-4
15	128.5	21.9	107	5	PCT-US95-16144-4
16	117.5	20.0	107	1	US-08-352-324A-7
17	117.5	20.0	107	2	US-08-862-607-7
18	117.5	20.0	107	2	US-08-468-819-5
19	117.5	20.0	107	3	US-09-203-235-7
20	117.5	20.0	107	5	PCT-US95-16144-7
21	113	19.3	71	2	US-08-812-003-9
22	109	18.6	106	4	US-08-679-493A-148
23	107	18.2	106	2	US-08-352-324A-5
24	107	18.2	106	2	US-08-862-607-5
25	107	18.2	106	2	US-08-468-819-7
26	107	18.2	106	3	US-09-203-235-5
27	107	18.2	106	5	PCT-US95-16144-5

28	99.5	17.0	73	2	US-08-436-420-42	Sequence 42, Appl
29	99.5	17.0	74	3	US-08-476-376-3	Sequence 3, Appl1
30	97	16.5	96	4	US-08-679-493A-147	Sequence 147, App
31	95.5	16.3	78	2	US-08-436-420-38	Sequence 38, Appl
32	94.5	16.1	126	1	US-07-624-742-1	Sequence 1, Appl1
33	93.5	15.9	77	2	US-08-436-420-39	Sequence 39, Appl
34	88.5	15.2	72	2	US-08-436-420-43	Sequence 43, Appl
35	88.5	15.1	72	3	US-08-846-966-1	Sequence 1, Appl1
36	88.5	15.1	72	3	US-08-557-142-1	Sequence 1, Appl1
37	88.5	15.1	72	5	PCT-US94-06264-1	Sequence 41, Appl1
38	88.5	15.1	77	2	US-08-436-420-41	Sequence 41, Appl
39	88	15.0	101	5	PCT-US95-16144-8	Sequence 8, Appl1
40	87.5	14.9	73	1	US-07-792-988-3	Sequence 3, Appl1
41	87.5	14.9	73	1	US-07-778-413E-19	Sequence 19, Appl
42	87.5	14.9	73	1	US-08-340-102-19	Sequence 19, Appl
43	87.5	14.9	73	2	US-08-436-420-27	Sequence 27, Appl
44	87.5	14.9	73	3	US-08-846-966-3	Sequence 3, Appl1
45	87.5	14.9	73	5	PCT-US94-06264-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-825-556A-2
; Sequence 2, Application US/08825556A
; Patent No. 5910431
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Su, Jeffrey Y.
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Chemokine Alpha 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-2934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,556A
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,653
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488, 0850001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-825-556A-2

Query Match 99.1%; Score 582; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 8.6e-64;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSLLPRAPVSMRLAALLLLALTYARVDGSKCKSRKGPRIKIRYSDVKLEMKPKY 60
 DB 1 MSLLPRAPVSMRLAALLLLALTYARVDGSKCKSRKGPRIKIRYSDVKLEMKPKY 60
 QY 61 PHCEKVVITTKSVSRIRGOEHLHPKLOSTKRFIKWYNAWNEKRRVYEE 111
 DB 61 PHCEKVVITTKSVSRIRGOEHLHPKLOSTKRFIKWYNAWNEKRRVYEE 111

RESULT 2

US-08-825-556A-3
 ; Sequence 3, Application US/08825556A
 ; Patent No. 5910431

GENERAL INFORMATION:

APPLICANT: Ni, Jian
 APPLICANT: Gentz, Reiner L.
 APPLICANT: Su, Jeffrey Y.
 APPLICANT: Li, Haodong
 TITLE OF INVENTION: Chemokine Alpha 2
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 STREET: 1100 New York Ave., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-2934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/825,556A
 FILING DATE: 19-MAR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013,653
 FILING DATE: 19-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0850001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 99 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-825-556A-3

Query Match

Best Local Similarity 99.0%; Score 522; DB 2; Length 99;
 Matches 99; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MRLIAALLLLALTYARVDGSKCKSRKGPRIKIRYSDVKLEMKPKYPHCEKVVITTT 72
 DB 1 MRLIAALLLLALTYARVDGSKCKSRKGPRIKIRYSDVKLEMKPKYPHCEKVVITTT 60
 QY 73 KVSRYRGOEHLHPKLOSTKRFIKWYNAWNEKRRVYEE 111
 DB 61 KVSRYRGOEHLHPKLOSTKRFIKWYNAWNEKRRVYEE 99

RESULT 3

US-09-188-930-344
 ; Sequence 344, Application US/09188930A
 ; Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James Greg
 TITLE OF INVENTION: Compositions Isolated From Skin Cells
 TITLE OF INVENTION: and Methods For Their Use
 FILE REFERENCE: 11000.1011cl
 CURRENT APPLICATION NUMBER: US/09/188,930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 344
 LENGTH: 95
 TYPE: PRT
 ORGANISM: Mouse
 US-09-188-930-344

Query Match

Best Local Similarity 86.7%; Score 509; DB 4; Length 95;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AALLLLALTYARVDGSKCKSRKGPRIKIRYSDVKLEMKPKYPHCEKVVITTKSVS 76
 DB 1 AALLLLALTYARVDGSKCKSRKGPRIKIRYSDVKLEMKPKYPHCEKVVITTKSVS 60

QY 77 RYRGOEHLHPKLOSTKRFIKWYNAWNEKRRVYEE 111
 DB 61 RYRGOEHLHPKLOSTKRFIKWYNAWNEKRRVYEE 95

RESULT 4

US-09-188-930-340
 ; Sequence 340, Application US/09188930A
 ; Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Onrust, Rene

APPLICANT: Murison, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 11000.1011cl

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 340

LENGTH: 99

TYPE: PRT

ORGANISM: Mouse

US-09-188-930-340

Query Match

Best Local Similarity 86.2%; Score 506; DB 4; Length 99;
 Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 13 MRLIAALLLLALTYARVDGSKCKSRKGPRIKIRYSDVKLEMKPKYPHCEKVVITTT 72
 DB 1 MRLIAALLLLALTYARVDGSKCKSRKGPRIKIRYSDVKLEMKPKYPHCEKVVITTT 60
 QY 73 KVSRYRGOEHLHPKLOSTKRFIKWYNAWNEKRRVYEE 111
 DB 61 KVSRYRGOEHLHPKLOSTKRFIKWYNAWNEKRRVYEE 99

RESULT 5

US-09-188-930-346
 ; Sequence 346, Application US/09188930A
 ; Patent No. 6150502

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; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-346
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Query Match          72.9%: Score 428; DB 4; Length 77;
Best Local Similarity 100.0%: Pred. No. 3.5e-45;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 35 SKCKSRKGRPIRYSVDVKLEMKPKYPHCEKMYITTKSVSRYGQEHCLHPKLOSTKR 94
|||||
DB 1 SKCKSRKGRPIRYSVDVKLEMKPKYPHCEKMYITTKSVSRYGQEHCLHPKLOSTKR 60
|||||
QY 95 FIKWYNAMNEKRYEE 111
|||||
DB 61 FIKWYNAMNEKRYEE 77
|||||
```

```
RESULT 6
US-09-188-930-345
; Sequence 345, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 345
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-345
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Query Match          72.2%: Score 424; DB 4; Length 77;
Best Local Similarity 97.4%: Pred. No. 1.1e-44;
Matches 75; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 35 SKCKSRKGRPIRYSVDVKLEMKPKYPHCEKMYITTKSVSRYGQEHCLHPKLOSTKR 94
|||||
DB 1 SKCKSRKGRPIRYSVDVKLEMKPKYPHCEKMYITTKSVSRYGQEHCLHPKLOSTKR 60
|||||
QY 95 FIKWYNAMNEKRYEE 111
|||||
DB 61 FIKWYNAMNEKRYEE 77
|||||
```

```
RESULT 7
US-09-188-930-157
; Sequence 157, Application US/09188930A
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; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 157
; LENGTH: 133
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-157
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Query Match          50.8%: Score 298; DB 4; Length 133;
Best Local Similarity 63.7%: Pred. No. 5.2e-29;
Matches 65; Conservative 6; Mismatches 25; Indels 6; Gaps 1;
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QY 13 MRLAALLLLALATYARVDSKCKSRKGRPIRYSVDVKLEMKPKYPHCEKMYITTK 72
|||||
DB 1 MRLAALLLLALATYARVDSKCKSRKGRPIRYSVDVKLEMKPKYPHCEKMYITTK 60
|||||
QY 73 KVSRYRGOE-----HCLHPKLOSTKRFIKWYNAMNEKRY 108
|||||
DB 61 KHVQGTGAKSTACTLSCRAPNASSGTMPTGTSAGSTNRV 102
|||||
```

```
RESULT 8
US-08-825-556A-4
; Sequence 4, Application US/08825556A
; Patent No. 5910431
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Su, Jeffrey Y.
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Chemokine Alpha 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-2934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,556A
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,653
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0850001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
```


ADDRESS: Incyte Pharmaceuticals, Inc.	
STREET: 3174 Porter Drive	
CITY: Palo Alto	
STATE: CA	
COUNTRY: US	
ZIP: 94304	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Diskette	
COMPUTER: IBM Compatible	
OPERATING SYSTEM: DOS	
SOFTWARE: FastSeq Version 1.5	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/862,607	
FILING DATE: 23-MAY-1997	
CLASSIFICATION: 435	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: 08/352,324	
FILING DATE: 07-DEC-1994	
ATTORNEY/AGENT INFORMATION:	
NAME: Luther, Barbara J.	
REGISTRATION NUMBER: 33,954	
REFERENCE/DOCKET NUMBER: PF-0025 US	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 415-855-0555	
TELEFAX: 415-852-0195	
INFORMATION FOR SEQ ID NO: 4:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 107 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: peptide	
US-08-862-607-4	
Query Match	21.9%; Score 128.5; DB 2; Length 107;
Best Local Similarity	33.3%; Pred. No. 2e-08;
Matches	42; Conservative 18; Mismatches 35; Indels 11; Gaps 2.
QY	8 APYVSMRLAALALLLALALYARVDG-----KCKCSRGRPKIRYSDVKLEMPKYP 61
DB	8 AANSNPLRLRVALLLLLVASRRAGAPLATELRCQCLQTLGSHLNKIQSVKVASPGP 67
QY	62 HCEKNVITTKSVSRRYRGQEHCLHPKIQSTKRFK 97
DB	68 HCAQTEVIATLKN----GQKACLNPASPMVKILIE 98
RESULT	13
US-08-468-819-6	
Sequence 6, Application US/08468819	
Patent No. 15871723	
GENERAL INFORMATION:	
APPLICANT: Strieter, Robert M.	
APPLICANT: Pulverini, Peter J.	
APPLICANT: Kunkel, Steven L.	
TITLE OF INVENTION: CXK Chemokines as Regulators of	
TITLE OF INVENTION: Angiogenesis	
NUMBER OF SEQUENCES: 93	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Arnold, White & Durkee	
STREET: P.O. Box 4433	
CITY: Houston	
STATE: TX	
COUNTRY: US	
ZIP: 77210	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: Patent Release #1.0, Version #1.30	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/468,819	

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1 FILING DATE: Concurrently herewith
2
3 CLASSIFICATION: 424
4
5 ATTORNEY/AGENT INFORMATION:
6
7 NAME: Highlander, Steven L.
8
9 REGISTRATION NUMBER: 37,642
10
11 REFERENCE/DOCKET NUMBER: UMIC.003/HYI
12
13 TELECOMMUNICATION INFORMATION:
14
15 TELEPHONE: 512/418-3000
16
17 TELEFAX: 512/474-7477
18
19 TELEX: N/A
20
21 INFORMATION FOR SEQ ID NO: 6:
22
23 SEQUENCE CHARACTERISTICS:
24
25 LENGTH: 107 amino acids
26
27 TYPE: amino acid
28
29 STRANDEDNESS: single
30
31 TOPOLOGY: linear
32
33 MOLECULE TYPE: peptide
34
35 OS-08-468-819-6

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Query Match	21.9%	Score 128.5;	DB 2;	Length 107;
Best Local Similarity	33.3%	Pred. No. 2e-08;		
Matches 32; Conservative	18;	Mismatches 35;	Indels 11;	Gaps 2

[illegible]

RESULT 14
US-09-203-235-4
Sequence 4, Application US/09203235
Patent No. 6071701
GENERAL INFORMATION:
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig C.
APPLICANT: Sellhammer, Jeffrey J.
TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/203.235
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862.607
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: 08/352.324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0025 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195

```

; INFORMATION FOR SEQ ID NO: 4
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 107 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
US-09-203-235-4

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Query Match	21.9%	Score 128.5;	DB 3;	Length 107;
Best Local Similarity	33.3%	Pred. No. 2e-08;		
Matches 32; Conservative	18;	Mismatches 35;	Indels 11;	Gaps 2

[illegible]

RESULT 15
PCT-US95-16144-4
; Sequence 4, Application PC/TUS9516144

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1  TITLE OF INVENTION:  A NOVEL CHEMOKINE EXPRESSED IN INFLAMED
2  TITLE OF INVENTION:  ADENOID, ITS PRODUCTION AND USES
3  NUMBER OF SEQUENCES:  9
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
6  STREET:  3174 Porter Drive
7  CITY:  Palo Alto
8  STATE:  CA
9  COUNTRY:  USA
10 ZIP:  94304
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE:  Floppy disk
13 COMPUTER:  IBM PC compatible
14 OPERATING SYSTEM:  PC-DOS/MS-DOS
15 SOFTWARE:  wordperfect 6.1/MS-DOS 6.2
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER:  PCT/US95/16144
18 FILING DATE:  07-DEC-1995
19 CLASSIFICATION:
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER:  US 08/352,324
22 FILING DATE:  07-DEC-1994
23 ATTORNEY/AGENT INFORMATION:
24 NAME:  LUTHER, BARBARA J.
25 REGISTRATION NUMBER:  33954
26 REFERENCE/DOCKET NUMBER:  PE-0025 PCT
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE:  415-855-0555
29 TELEFAX:  415-852-0195
30 INFORMATION FOR SEQ ID NO:  4:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH:  107 amino acids
33 TYPE:  amino acid
34 STRANDEDNESS:  single
35 TOPOLOGY:  linear
36 MOLECULE TYPE:  protein
37
38 PCT-US95-16144-4

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Query Match      21.9%; Score 128.5; DB 5; Length 107;
Best Local Similarity 33.3%; Pred. No. 2e+08;
Matches 32; Conservative 18; Mismatches 35; Indels 11; Gaps 2;

QY      8 APVPSRLLAALLLLLLALTYARDGS-----KCCCKSRKGRKIRSDYKCKLEMKPKYP 61
      | | : | | | | | | | | | | : | : | : | : | : | : | : | : |

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Wed Jan 30 09:49:25 2002

us-09-978-189-370.ra1

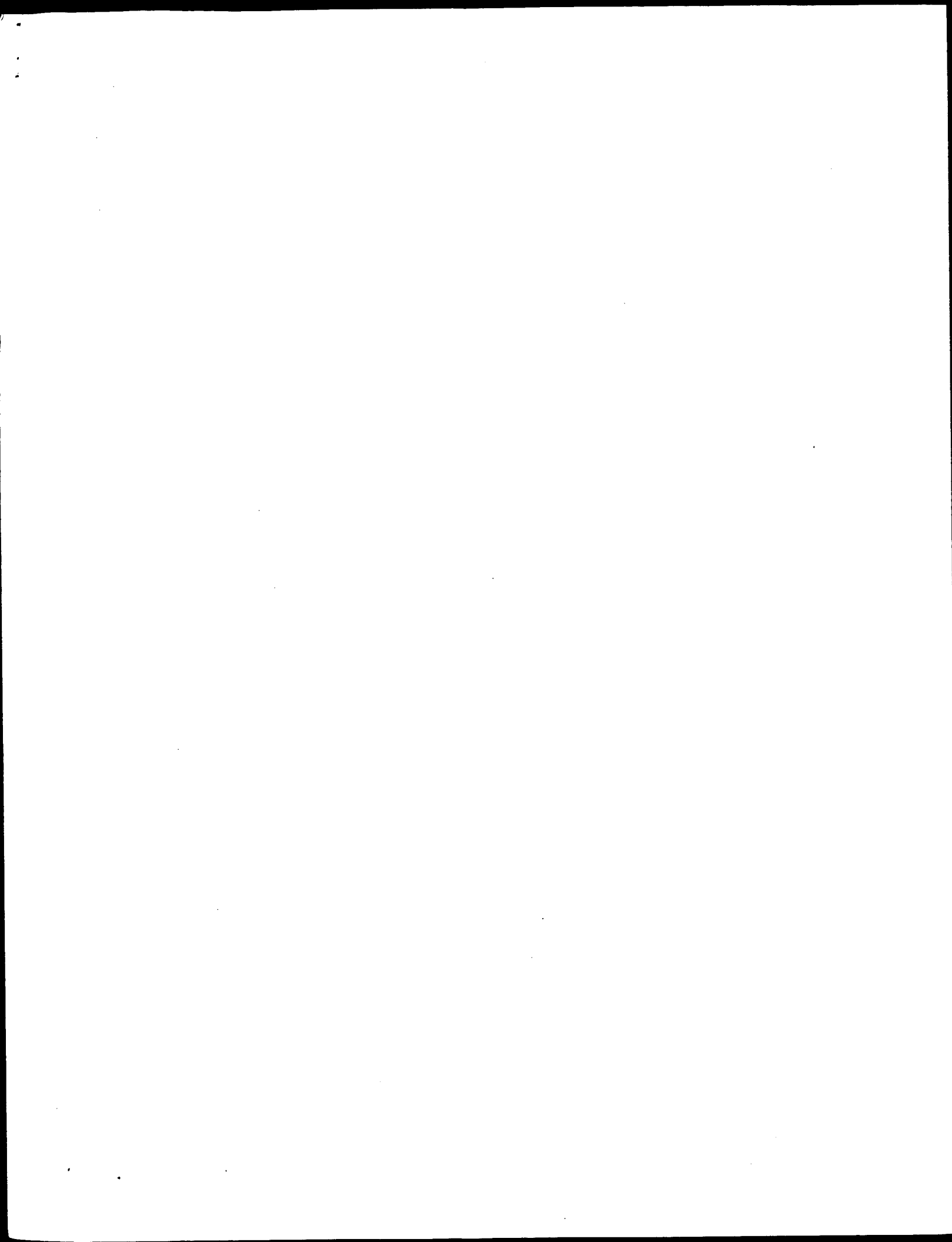
Page 7

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QY 62 HCEKMVIITKSVSRVRYRQGEHCLPKIQTSTREIK 97

Db 68 HCAQTEVIATLKN----GQKCLNPASPMPWKILTE 98

Search completed: January 29, 2002, 16:04:25
Job time: 51 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 14.34 Seconds

(without alignments)
589,636 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 587

Sequence: 1 MSLLPRAPPVSMRLAAL.....TKRFIKYNAWNEKRYVEE 111

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520	88.6	99	2	JG0182
2	143.5	24.4	100	2	S46198
3	138	23.5	100	2	JH0200
4	131	22.3	101	2	B28414
5	128.5	21.9	107	2	JH0281
6	124	21.1	100	2	S21467
7	117.5	20.0	107	2	A28414
8	117.5	19.8	107	2	B38290
9	116.5	19.8	107	2	A32954
10	111	18.9	96	2	A32954
11	103	17.5	117	2	B44253
12	97	16.5	96	2	JN0572
13	94.5	16.1	126	2	A35766
14	87.5	14.9	125	2	JN0470
15	85.5	14.6	53	2	I51866
16	84	14.3	104	1	PFH04A
17	82.5	14.1	103	2	A53096
18	82.5	14.1	128	1	TGHU
19	81.5	13.9	95	2	JN0841
20	81	13.8	101	1	PFH04
21	80.5	13.7	53	2	I64831
22	80.5	13.7	98	2	A45492
23	80.5	13.7	103	2	A26736
24	80.5	13.7	103	2	I50417
25	80	13.6	119	2	S42881
26	79.5	13.5	98	1	TGHUG1
27	79.5	13.5	101	2	S42496
28	76.5	13.0	114	2	A55010
29	76	12.9	132	2	A57325

ALIGNMENTS

30	76	12.9	677	2	T27127	hypothetical prote
31	74	12.6	394	2	T32670	hypothetical prote *
32	73.5	12.5	75	2	A54188	granulocyte chemot
33	79	12.4	105	2	A26774	platelet factor 4
34	72.5	12.4	101	2	I46871	interleukin-8 - ra
35	71.5	12.2	75	2	B54188	granulocyte chemot
36	71	12.1	99	2	A37034	interleukin-8 prec
37	71	12.1	1270	2	T28087	hypothetical prote
38	70	11.9	308	1	S76941	carbamate kinase (
39	69.5	11.8	98	2	I59277	Mob-1 - rat
40	69.5	11.8	807	1	I51685	replication licens
41	68	11.6	149	2	T25246	hypothetical prote
42	68	11.6	309	2	S76393	hypothetical prote
43	68	11.6	581	2	C64251	flagella accessory
44	67.5	11.5	90	2	S69133	platelet factor 4
45	67	11.4	647	2	J60337	frizzled-1 protein

ALIGNMENTS

RESULT	1	
JG0182		
chemokine BRK - human		
C:Species: Homo sapiens (man)		
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000		
C:Accession: JG0182		
R:Thomas, R.; Brommeyer, H.E.; Kim, C.; Nakshatri, H.; Christopherson II, K.; Hou, Y.		
Biochem. Biophys. Res. Commun. 255, 703-706, 1999		
A:Title: Cloning of BRK, a novel divergent CXC chemokine preferentially expressed in		
A:Reference number: JG0182; MUID:99160416		
A:Accession: JG0182		
A:Status: preliminary		
A:Molecule type: mRNA		
A:Residues: 1-99 <HRO>		
A:Cross-references: GB:AF073957		
C:Superfamily: beta-thromboglobulin		

Query Match	88.6%;	Score 520;	DB 2;	Length 99;
Best Local Similarity	99.0%;	Pred. No. 3.2e-47;		
Matches 98; Conservative	0;	Mismatches 1;	Indels	0; Gaps 0;

QY	13	MRLAALLLLLLALYARVDGSKCKSRGPKIRYSDVKLEMKPKYPHCEKNVITTT	72
DB	1	MRLPAALLLLLLALYARVDGSKCKSRGPKIRYSDVKLEMKPKYPHCEKNVITTT	60
QY	73	KSVSRVSGEHCILHPKLOSTKRFIKYNAWNEKRYVEE	111
DB	61	KSVSRVSGEHCILHPKLOSTKRFIKYNAWNEKRYVEE	99

RESULT	2	
S46198		
cytokine-induced neutrophil chemoattractant 2 - rat		
C:Species: Rattus norvegicus (Norway rat)		
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000		
C:Accession: S46198; C48988		
R:Nakagawa, H.; Komorita, N.; Shibata, F.; Ikese, A.; Konishi, K.; Fujioaka, M.; Kato		
Biochem. J. 301, 545-550, 1994		
A:Title: Identification of cytokine-induced neutrophil chemoattractants (CINC), rat G		
ences and characterization.		
A:Reference number: S46198; MUID:94318061		
A:Accession: S46198		
A:Status: preliminary		
A:Molecule type: mRNA		
A:Residues: 1-100 <NAK>		
A:Cross-references: EMBL:D21095; NID:G517143; PIDN:BA04657.1; PID:G517144		
R:Nakagawa, H.; Ikese, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watan		
Biochem. Pharmacol. 45, 1425-1430, 1993		
A:Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK		
A:Reference number: A48988; MUID:93228656		
A:Accession: C48988		

hypothetical prote
granulocyte chemot
platelet factor 4
interleukin-8 - ra
granulocyte chemot
interleukin-8 prec
hypothetical prote
carbamate kinase (
Mob-1 - rat
replication licens
hypothetical prote
hypothetical prote
flagella accessory
platelet factor 4
frizzled-1 protein

A>Status: preliminary
A:Molecule type: protein
A:Residues: 33-56 <NA2>
A:Experimental source: kidney, NRK-49F fibroblasts
A>Note: sequence extracted from NCBI backbone (NCBIP:129130)
C:Superfamily: beta-thromboglobulin

Query Match 24.4%; Score 143.5; DB 2; Length 100;
Best Local Similarity 35.1%; Pred. No. 5.9e-08;
Matches 34; Conservative 19; Mismatches 31; Indels 13; Gaps 3;

QY 8 APPVSMRLAALALLLLALTYARVDG-----KCKCSRKGPRIKRYSDVKLEMPKPY 60
DB 2 APP-TRRLNALALLLLLMATSHQPSGTAVARLRQCCKLTLPVDFENIGSLTYTPPG 60

QY 61 PCEKMYITTKSVSRVSGOEHCHPKLOSTKRFK 97
DB 61 PCTQTEVIATLKD-----GQEVCLNPEAPRLQKIQQ 92

RESULT 3
JH0200
macrophage inflammatory protein 2 precursor - mouse

C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C:Accession: JH0200; A32190

R:Ekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev
J. Exp. Med. 172, 911-919, 1990

A:Title: Cloning and characterization of cDNAs for murine macrophage inflammatory protei
A:Reference number: JH0200; MUID:90354792

A:Accession: JH0200

A:Molecule type: mRNA
A:Residues: 1-100 <TEK>

A:Cross-references: GB:X53798; NID:953128; PIDN:CAA37807.1; PID:953129
R:Wolpe, S.D.; Sherry, B.; Juers, D.; Davatelis, G.; Yurt, R.W.; Cerami, A.

Proc. Natl. Acad. Sci. U.S.A. 86, 612-616, 1989

A:Title: Identification and characterization of macrophage inflammatory protein 2.

A:Reference number: A32190; MUID:89098980

A:Accession: A32190

A:Molecule type: protein
A:Residues: 28-59 <WOL>

C:Superfamily: beta-thromboglobulin
C:Keywords: heparin binding

F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-100/Product: macrophage inflammatory protein 2 #status experimental <MAT>

Query Match 23.5%; Score 138; DB 2; Length 100;
Best Local Similarity 33.3%; Pred. No. 2.2e-07;
Matches 32; Conservative 21; Mismatches 31; Indels 12; Gaps 3;

QY 8 APPVSMRLAALALLLLALTYARVDG-----KCKCSRKGPRIKRYSDVKLEMPKPY 61
DB 2 APP-TRRLNALALLLLLMATSHQPSGTAVARLRQCCKLTLPVDFENIGSLTYTPPG 60

QY 62 HCEKMYITTKSVSRVSGOEHCHPKLOSTKRFK 97
DB 61 HCAQTEVIATLKG-----GQKVCIDPEAPRLQKIQQ 91

RESULT 4

B28414
growth-regulated protein precursor - Chinese hamster

C:Species: Crithideus griseus (Chinese hamster)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C:Accession: B28414

R:Anisowicz, A.; Bardwell, L.; Sager, R.

Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987

A:Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese h
A:Reference number: A94184; MUID:88041072

A:Accession: B28414
A:Molecule type: mRNA

A:Residues: 1-101 <ANT>
A:Cross-references: GB:J03560; NID:9191088; PIDN:AAA6985.1; PID:9304509
A>Note: the authors translated the codon CAG for residue 52 as GGU
C:Superfamily: beta-thromboglobulin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-101/Product: growth-regulated protein #status predicted <MAT>

Query Match 22.3%; Score 131; DB 2; Length 101;
Best Local Similarity 31.6%; Pred. No. 1.2e-06;
Matches 30; Conservative 21; Mismatches 32; Indels 12; Gaps 2;

QY 10 PVSRLAALALLLLALTYARV-----DQSKCSRKGPRIKRYSDVKLEMPKPY 62
DB 3 PATRLRLRPLLLLLATSLRAGAPVAPNLRQCCKLTLPVDFENIGSLTYTPPG 62

QY 63 CEKMYITTKSVSRVSGOEHCHPKLOSTKRFK 97
DB 63 CTQTEVIATLKN-----GQEVCLNPEAPRLQKIQQ 92

RESULT 5
JH0281
macrophage inflammatory protein 2 alpha precursor - human

N:Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulato
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C:Accession: JH0281; A35931; A38290; A60407

R:Ekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van
J. Exp. Med. 172, 911-919, 1990

A:Title: Cloning and characterization of cDNAs for murine macrophage inflammatory pro
A:Reference number: JH0200; MUID:90354792

A:Accession: JH0281

A:Molecule type: mRNA
A:Residues: 1-107 <TEK>

A:Cross-references: GB:X53799; NID:934658; PIDN:CAA37808.1; PID:934659
R:Ridd, N.; Grotenordt, G.R.

Mol. Cell. Biol. 10, 5596-5599, 1990

A:Title: Cloning and sequencing of a new gro transcript from activated human monocyte
A:Reference number: A35931; MUID:90377255

A:Accession: A35931

A:Molecule type: mRNA
A:Residues: 1-107 <IID>

A:Cross-references: GB:M57731; GB:M36964; NID:9183626; PIDN:AAA63183.1; PID:9183627
R:Haskill, S.; Pearce, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T

Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990

A:Title: Identification of three related human GRO genes encoding cytokine functions.
A:Reference number: A38290; MUID:91017578

A:Accession: A38290

A:Molecule type: mRNA
A:Residues: 1-107 <HAS>

A:Cross-references: GB:M36820; NID:9183628; PIDN:AAA63183.1; PID:9183629
R:Sporn, S.A.; Elerman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Hask

J. Immunol. 144, 4434-4441, 1990

A:Title: Monocyte adherence results in selective induction of novel genes sharing hom

A:Reference number: A60407; MUID:90257367

A:Accession: A60407

A:Molecule type: mRNA
A:Status: not compared with conceptual translation

A:Residues: 56-107 <SPO>
C:Superfamily: beta-thromboglobulin

C:Keywords: inflammation
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <MAT>

Query Match 21.9%; Score 128.5; DB 2; Length 107;
Best Local Similarity 33.3%; Pred. No. 2.3e-06;
Matches 32; Conservative 18; Mismatches 35; Indels 11; Gaps 2;

QY 8 APPVSMRLAALALLLLALTYARVDG-----KCKCSRKGPRIKRYSDVKLEMPKPY 61
DB 8 AAPSNRLLRVALLLLLLVASRAAGAPLATELRCQCLQTLQGIHLKNIQSVKVKSPGP 67

OY 62 HCEKMWITTKSVRYGEOHCLHPKLOSTKREIK 97
 Db 68 HCAQTEVIATLKND-----GQKACLNPPASPMVKRIIE 98

RESULT 6

S21467
 macrophage inflammatory protein 2 - rat
 N:Alternate names: chemoattractant P-1
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
 C:Accession: S21467; D48988
 R:Discooll, K.
 Submitted to the EMBL Data Library, April 1992
 A:Reference number: S21467
 A:Accession: S21467
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1100 <DR1>
 A:Cross-references: EMBL:X65647; NID:956665; PIDN:CAA46599.1; PID:956666
 R:Nakagawa, H.; Ikeue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanabe
 Biochem. Pharmacol. 45, 1425-1430, 1993
 A>Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-49
 A:Reference number: A48988; MUID:93228656
 A:Accession: D48988
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 32-45 <NAK>
 A:Experimental source: kidney, NRK-49F fibroblasts
 A:Note: sequence extracted from NCBI backbone (NCBIP:129129)
 C:Superfamily: beta-thromboglobulin

Query Match 21.1%; Score 124; DB 2; Length 100;
 Best Local Similarity 33.7%; Pred. No. 6.3e-06;

Matches 32; Conservative 16; Mismatches 37; Indels 10; Gaps 3;

OY 8 APPVSRMLAALALLLLALY---TARVDS--KCKSRKPKIRYSDVKLEMKPKYPH 62
 Db 2 APPTRQLNNAVILVLLLLATNHOGTGVVASELRCCQLTTLPRVDFKNIQSLTVTPPGPH 61

OY 63 CEKMWITTKSVRYGEOHCLHPKLOSTKREIK 97
 Db 62 CAQTEVIATLKND-----GHEVCLNPPAPLVQRIIVQ 91

RESULT 7

S215614
 macrophage inflammatory protein-2 - rat
 C:Species: Rattus sp. (rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
 C:Accession: I55614
 R:Feng, L.; Xia, Y.; Yoshimura, T.; Wilson, C.B.
 J. Clin. Invest. 95, 1009-1017, 1995
 A>Title: Modulation of neutrophil influx in glomerulonephritis in the rat with anti-macr
 A:Reference number: I55614; MUID:95189993
 A:Accession: I55614
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-100 <RES>
 A:Cross-references: GB:S77604; NID:9998406; PIDN:AAB33749.1; PID:9998407
 C:Superfamily: beta-thromboglobulin

Query Match 21.1%; Score 124; DB 2; Length 100;
 Best Local Similarity 33.7%; Pred. No. 6.3e-06;

Matches 32; Conservative 16; Mismatches 37; Indels 10; Gaps 3;

OY 8 APPVSRMLAALALLLLALY---TARVDS--KCKSRKPKIRYSDVKLEMKPKYPH 62
 Db 2 APPTRQLNNAVILVLLLLATNHOGTGVVASELRCCQLTTLPRVDFKNIQSLTVTPPGPH 61

OY 63 CEKMWITTKSVRYGEOHCLHPKLOSTKREIK 97
 Db 62 CAQTEVIATLKND-----GHEVCLNPPAPLVQRIIVQ 91

RESULT 8

A28414
 melanoma growth-stimulatory activity precursor - human
 N:Alternate names: fibroblast-derived neutrophil-activating protein gamma; GRO-alpha;
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
 C:Accession: S13669; A28414; S00983; B60401; S03976; A47626; B46519
 R:Baker, N.E.; Kucera, G.; Richmond, A.
 Nucleic Acids Res. 18, 6453, 1990
 A>Title: Nucleotide sequence of the human melanoma growth stimulatory activity (MGS)
 A:Reference number: S13669; MUID:91057157
 A:Accession: S13669
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-107 <BAR>
 A:Cross-references: EMBL:X54489; NID:934625; PIDN:CAA38361.1; PID:934626
 R:Antisowicz, A.; Bardwell, L.; Sager, R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
 A>Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese
 A:Reference number: A94184; MUID:88041072
 A:Accession: A28414
 A:Molecule type: mRNA
 A:Residues: 1-107 <ANT>
 A:Cross-references: GB:J03561; NID:9183622; PIDN:AAA35933.1; PID:9306806
 R:Richmond, A.; Balenlien, E.; Thomas, H.G.; Flagg, G.; Barton, D.E.; Spiess, J.; Bo
 EMBO J. 7, 2025-2033, 1988
 A>Title: Molecular characterization and chromosomal mapping of melanoma growth stimu
 A:Reference number: S00983; MUID:88328991
 A:Accession: S00983
 A:Molecule type: mRNA
 A:Residues: 1-107 <RIC>
 A:Cross-references: EMBL:X12510; NID:934621; PIDN:CAA31027.1; PID:934622
 R:Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E
 J. Immunol. 144, 2223-2232, 1990
 A>Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL
 A:Reference number: A60401; MUID:90187866
 A:Accession: B60401
 A:Molecule type: protein
 A:Residues: 35-42, 'X', '44', 'X', '46-48 <SCH>
 A:Experimental source: dermal fibroblasts
 R:Golds, E.E.; Mason, P.; Nyirkos, P.
 Biochem. J. 259, 585-588, 1989
 A>Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a n
 A:Reference number: S03975; MUID:89246368
 A:Accession: S03976
 A:Molecule type: protein
 A:Residues: 35-41, 'X', '43-49', 'X', '51-52', 'XX', '55-57 <GOL>
 R:Schroeder, J.M.; Peterson, N.L.M.; Christophers, E.
 J. Exp. Med. 171, 1091-1100, 1990
 A>Title: Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil
 nity with melanoma growth stimulatory activity.
 A:Reference number: A47626; MUID:90217938
 A:Accession: A47626
 A:Molecule type: protein
 A:Residues: 35-63, 'X', '65 <SC2>
 A:Experimental source: LPS-stimulated monocytes
 R:Pirot, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damm
 J. Immunol. 150, 1000-1010, 1993
 A>Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human
 A:Reference number: A46519; MUID:9139489
 A:Accession: B46519
 A:Molecule type: protein
 A:Residues: 35-62 <PRO>
 A:Experimental source: MG-63 osteosarcoma cells
 C:Genetics:
 A:Gene: GDB:GR01
 A:Cross-references: GDB:120181; OMIM:155730
 A:Map position: 4q21-4q21

JN0572

A:Residues: 1-96 <KON>
A:Cross-references: DDBJ:D11445; NID:9391854; PIDD:BAA02009.1; PID:q220755
R: Huang, S.; Paulauskis, J.D.; Kobzik, L.
Biochem. Biophys. Res. Commun. 184, 922-929, 1992
A:Title: Rat KC CDNA cloning and mRNA expression in lung macrophages and fibroblasts
A:Reference number: J01519; MUID:92246987
A:Accession: J01519
A:Molecule type: mRNA
A:Residues: 132, 'S', 34-96 <HUA>
A:Cross-references: GB:M86536

A, 111116: The neutrophil chemoattractant produced by the rat kidney epithelioid cell line A, Reference number: A34481; MUID: 90062049

A:Accession: A34481
A:Molecule type: protein
A:Residues: 25-96 <MAT>
A:Ubiquitous: 0

A:Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NK-49
A:Reference number: A4988; MID:93228656
A:Accession: 14980

A: accession: A46568
A: Status: preliminary
A: Molecule type: protein
A: peptides: 35-57 <unk>

A: Experimental source: kidney, NRR-49F fibroblasts
A: Note: sequence extracted from NCBI backbone (NCBI:129132)

A:Accession: B46968
A:Status: preliminary
A:Molecule type: protein
A:Position: 3657-4093

A:Residues: 23-57 / <MA2>
A:Experimental source: kidney, NRK-49F fibroblasts
A:Note: sequence extracted from NCBI backbone (NCBIP:129131)

Address: The three dimensional structure of rat cytokine CINC/Gro in solution by homonud

A:reference number: S51214; MUID:95046335
A:Contents: annotation; conformation by (1)H-NMR, residues 25-96
A:Accession: S51214

Comment: This protein has chemotactic activity for neutrophils and has melanoma growth promoting activity.

C:genetics: KC
A:Gene: gro: KC
A:Introns: 24/1; 65/2; 92/2

C:superfamily: beta-thromboglobulin
C:Keywords: cytokine; disulfide bond
F1-24/Domain: signal sequence #status predicted <SIG>

Product: neutrophil chemo-attractant Gro protein #stratus experimental <CXT>

Query Match	16.5%	Score 97 ; DB 2 :	Length 96 ;
Best Local Similarity	27.8%	Pred. No. 0.004 :	
Matches 25 ; Conservative	20 ; Mismatches	29 ; Indels	16 ; Gaps 3 ;

[illegible]

RESULT 13	
A35766	

C:Species: Mus musculus (house mouse)
C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 20-Aug-1995
Accession: M35766
platelet factor 4, interferon gamma-induced, precursor - mouse

Proc. Natl. Acad. Sci. U.S.A. 87, 5238-5242, 1990

A:Reference number: A35766; MUID:90319087
A:Accession: A35766
A:Status: not submitted

A;Residues: 1-126 <FAR>
A;Molecule type: mRNA
A;Status: preliminary
A;Cross-reference: CD, M24015, WTD, J100603, NT01, J100705, E22, J100603

C; Superfamily: beta-thromboglobulin
 REFERENCES: Q6:MC4815; MIM:619303Z; P1DN:AAA39/06.1; P1D:g199b93

Query Match	16.1%;	Score 94.5;	DB 2;	Length 126;
Best Local	Similarity 25.5%;	Pred. No. 0.0093;		
Matches	26;	Conservative 21;	Mismatches 40;	Indels 15; Gaps

16 LAALLLLLLLY-----TAVDGSKKCC-SRKGPRIYSDVKLEMPKYPHCEEK 66

D5 1 MNSAVLELMILFLEKCGVGILVIRNARCSISIKOTIHYSLEKLDKQFAPSPNENKT 60

QY 67 MYITTKSVSRYGQEHCHLPKLDSTKPTK-WYNNANEKRR 107

D5 61 E1ATLKN-----GDQTCLDPPDSANVKKLLKKEWEKKNQKKK 97

RESULT	14
JN0470	

C;Species: Homo sapiens (man)
interleukin gamma-induced protein HUMIG - human
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-May-1999
Accession: U04470

R;Farber, J.M.
Biochem. Biophys. Res. Commun. 192, 223-230, 1993

A;Title: A new human member of the chemokine family of cytokines.
A;Reference number: JN0470; MUID:9323577
A;Accession: JN0470

A; molecule type: mRNA
A; Residues: 1-125 <FAR>
A; Cross-references: GB:X72755; GB:S60728; NID:g311375; P1DN:CAA51284.1; PID

C/Superfamily: beta-thromboglobulin
C/Keywords: cytokine

Query Match	Score	DB 2	Length
Best Local Similarity	14.9%	87.5	125
	29.5%	Pred. No.	0.05

Matches	28;	conservative	14;	Mismatches	46;	Indels	7;	Gaps	
QY	15	LLAALLLLLLA	LTARVDGSKKC-SRKGPKIRYSDVKKLEMKPKYPHCEEKWIITTK	73					

Db 9 LGGITLVIGVGTTPVVRKGRCSGISITNGTINLQSLKDLKQFAPSPSCKEIETATLK 68

QY /4 SVSRKRGQEHCLHPKLQSTKRFI-KWYNAMNEKKRR 107
 : | : || : | | : : | :
Db 69 N-----GVQTCLNPPDSADVKELIKRWKQVSQKKK 98

RESULT 15

macrophage inflammatory protein-2 - rat (fragment)
CISpecies: Rattus sp. (rat)

```

cdate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Feb-1997

```

C:Accession: 151886
R: Huang, S.; Paulauskis, J.D.; Godleski, J.J.; Kobzik, L.
Am. J. Pathol. 141, 981-988, 1992
A: Title: Expression of macrophage inflammatory protein-2 and KC mRNA in pulmonary inflammation
A: Reference number: 151886; MUID: 93035653
A: Accession: 151886
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-53 <RES>
A: Cross-references: GB:S45855; NID:q257054
C: Superfamily: beta-thromboglobulin

Query Match	14.6%	Score 85.5	DB 2	Length 53
Best Local Similarity	29.6%	Pred. No. 0.036		
Matches 16	Conservative 13	Mismatches 20	Indels 5	Gaps 1
OY	44	PKIRISVVKLEMKPKYPHCEKMTITTSKSRKRGCHLHKLSTSTRFK	97	
Db	5	PRDEKMSGLVITPPGHCAGLEVALIKD-----GHEVLINAEAPLVQRIYQ	53	

Search completed: January 29, 2002, 16:04:46
Job time: 72 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 11.67 Seconds
(without alignments)

348,740 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 587
Sequence: 1 MSLLPRRAPVSMRLAAL.....TKRFIKWYNAMEKRYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	527	89.8	99	1 SZ14_HUMAN	O95715 homo sapien
2	489	83.3	99	1 SZ14_MOUSE	Q9WU95 mus musculu
3	143.5	24.4	100	1 M12B_RAT	Q10747 rattus norv
4	138	23.5	100	1 M12P_MOUSE	P10889 mus musculu
5	131	22.3	101	1 GRO_CRIGR	P09340 cricetus
6	128.5	21.9	107	1 M12A_HUMAN	P19875 homo sapien
7	127.5	21.7	103	1 GRO_SHEEP	O46678 ovls aries
8	124	21.1	100	1 M1P2_RAT	P30348 rattus norv
9	122.5	20.9	98	1 GRO2_BOVIN	O46675 bos taurus
10	118.5	20.2	104	1 GRO2_RABIT	P47854 oryctolagus
11	117.5	20.0	104	1 GRO2_BOVIN	O46677 bos taurus
12	117.5	20.0	107	1 GRO_HUMAN	P09341 homo sapien
13	116.5	19.8	107	1 M12B_HUMAN	P19876 homo sapien
14	113.5	19.3	104	1 GROA_BOVIN	O46676 bos taurus
15	111	18.9	96	1 GRO_MOUSE	P12850 mus musculu
16	104.5	17.8	68	1 M12A_RAT	Q10746 rattus norv
17	103	17.5	104	1 GRO_CAVPO	O55235 cavia porce
18	103	17.5	117	1 AMC2_PIG	P22652 sus scrofa
19	97	16.5	96	1 GRO_RAT	P14095 rattus norv
20	94.5	16.1	126	1 SZ03_MOUSE	P18340 mus musculu
21	90.5	15.4	71	1 GROL_RABIT	P30782 oryctolagus
22	87.5	14.9	125	1 SZ06_HUMAN	O80162 homo sapien
23	87	14.8	114	1 SZ06_HUMAN	P80221 bos taurus
24	86	14.7	112	1 SZ06_BOVIN	O46625 homo sapien
25	84	14.3	94	1 SZ11_HUMAN	P10720 homo sapien
26	84	14.3	104	1 PLFY_HUMAN	P41324 canis famill
27	83.5	14.2	101	1 IL8_CANFA	P26894 sus scrofa
28	82.5	14.1	103	1 IL8_PIG	P02775 homo sapien
29	82.5	14.0	128	1 PF4L_HUMAN	O92558 homo sapien
30	82	14.0	94	1 SY26_HUMAN	P97685 rattus norv
31	82	14.0	130	1 SZ05_RAT	P02776 homo sapien
32	81	13.8	101	1 PLF4_HUMAN	P17515 mus musculu
33	80.5	13.7	98	1 SZ10_MOUSE	

34	80.5	13.7	101	1 IL8_BOVIN	P79255 bos taurus
35	80.5	13.7	103	1 EMF1_CHICK	P08317 gallus gall.
36	80	13.6	119	1 PF4L_PIG	P43030 sus scrofa
37	79.5	13.5	98	1 SZ10_HUMAN	P02778 homo sapien
38	79.5	13.5	101	1 IL8_SHEEP	P36925 ovls aries
39	76.5	13.0	114	1 SZ05_HUMAN	P42830 homo sapien
40	76	12.9	132	1 SZ05_MOUSE	P50228 mus musculu
41	75.5	12.9	97	1 IL8_HORSE	O62812 equus caball
42	73	12.4	89	1 SY18_HUMAN	P55774 h small ind
43	73	12.4	105	1 PLF4_RAT	P06765 rattus norv
44	72.5	12.4	101	1 IL8_RABIT	P19874 oryctolagus
45	72	12.3	101	1 IL8_MACMU	P51495 macaca mulia

ALIGNMENTS

RESULT	ID	STANDARD	PRT	99 AA
1	SZ14_HUMAN			
AC	O95715;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	SMALL INDUCIBLE CYTOKINE B14 PRECURSOR (CHEMOKINE BRK).			
GN	SCYB14 OR NJAC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99160416; PubMed=10049774;			
RA	Hromas R., Broxmeyer H.E., Kim C., Nakshatri H., Christopherson K. II,			
RA	Azam M., Hou Y.-H.;			
RT	"Cloning of BRK, a novel divergent CXK chemokine preferentially			
RT	expressed in normal versus malignant cells.";			
RL	Biochem. Biophys. Res. Commun. 255:703-706(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Oral epithelium;			
RA	Frederick M.F., Henderson Y., Xu X., El-Naggar A.K., Wu H.,			
RA	Hudson J.M., Clayman G.L.;			
RL	Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.			
CC	- FUNCTION: NOT CHEMOTACTIVE FOR T-CELLS, B-CELLS, MONOCYTES,			
CC	NATURAL KILLER CELLS OR GRANULOCYTES. DOES NOT INHIBIT			
CC	PROLIFERATION OF MYELOID PROGENITORS IN COLONY FORMATION ASSAYS.			
CC	- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUNG,			
CC	LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS. HIGHLY EXPRESSED IN			
CC	NORMAL TISSUE WITHOUT INFLAMMATORY STIMULI AND INFREQUENTLY			
CC	EXPRESSED IN CANCER CELL LINES.			
CC	- SIMILARITY: BELONGS TO THE INTERFERON ALPHA FAMILY (SMALL CYTOKINE			
CC	C-X-C) (CHEMOKINE CXC).			
CC	-----			
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CC	-----			
CC	EMBL: AF07957; AAD03839.1; -			
CC	EMBL: AF144103; AAD8944.1; -			
DR	MM: 604186; -			
DR	InterPro: IPR001811; Chemokine_IL8.			
DR	InterPro: IPR001089; Small_cytokine_CXC.			
DR	PRINTS: PR00436; INTERLEUKIN8.			
DR	SMART: SM00199; SCY; 1.			
DR	PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.			
KW	Cytokine; Signal.			
FT	SIGNAL 1 22			POTENTIAL.
FT	CHAIN 23 99			SMALL INDUCIBLE CYTOKINE B14.

FT DISULFID 25 51 BY SIMILARITY.
 FT DISULFID 27 72 BY SIMILARITY.
 SQ SEQUENCE 99 AA: 11772 MW: 998802D8FC659C1D CRC64;

Query Match 89.8%; Score 527; DB 1; Length 99;
 Best Local Similarity 100.0%; Pred. No. 2.8e-49;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 MRLAAALLLLLLALYTRAVDGSCKCKSRGPKIRYSDVKLEMKPKYPHCEKMWIYTT 72
 |||
 DB 1 MRLAAALLLLLLALYTRAVDGSCKCKSRGPKIRYSDVKLEMKPKYPHCEKMWIYTT 60

OY 73 KVSRYRGQEHCLHPKLGOSTRKRFIKWYNAMNEKRYEE 111
 |||
 DB 61 KVSRYRGQEHCLHPKLGOSTRKRFIKWYNAMNEKRYEE 99

RESULT 2

S214_MOUSE STANDARD; PRT; 99 AA.

AC 09W005;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SMALL INDUCIBLE CYTOKINE B14 PRECURSOR (CHEMOKINE BRAK) (KIDNEY-
 EXPRESSED CHEMOKINE CXC).
 OS SCYB14 OR KEC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RA Hromas R., Broxmeyer H.E., Kim C., Nakshatri H., Christopherson K. II,
 Azam M., Hou Y.-H.;
 RT "Cloning of BRAK, a novel divergent CXC chemokine preferentially
 expressed in normal versus malignant cells."
 RL Biochem. Biophys. Res. Commun. 255:703-706(1999).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H;

RA Wang L., Deng L., Raikwar N., Sahota A., Tischfield J.A.;

RT "Identification of a kidney-expressed chemokine (KEC), a member of the

CXC family, that is selectively elevated in apt knockout mice."

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases

-I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE

C-X-C) (CHEMOKINE CXC).

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EMBL: AF152377; AAD34157.1; -

EMBL: AF192557; AAF03753.1; -

DR MGD; MG1:1888514; Scybl4.

DR InterPro: IPR001811; Chemokine_IL8.

DR InterPro: IPR001089; Small_cytokine_CXC.

DR PRINTS: PRO0436; INTERLEUKIN8.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.

DR CYTOKINE; Signal.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 99 SMALL INDUCIBLE CYTOKINE B14.

FT DISULFID 25 51 BY SIMILARITY.

FT DISULFID 27 72 BY SIMILARITY.

FT CONFLICT 64 64 F -> S (IN REF. 2).

FT SEQUENCE 99 AA: 11802 MW: 754B6CDA01CA25D CRC64;

Query Match 83.3%; Score 489; DB 1; Length 99;
 Best Local Similarity 91.9%; Pred. No. 3e-45;
 Matches 91; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 13 MRLAAALLLLLLALYTRAVDGSCKCKSRGPKIRYSDVKLEMKPKYPHCEKMWIYTT 72
 |||
 DB 1 MRLAAALLLLLLALYTRAVDGSCKCKSRGPKIRYSDVKLEMKPKYPHCEKMWIYTT 60

OY 73 KVSRYRGQEHCLHPKLGOSTRKRFIKWYNAMNEKRYEE 111
 |||
 DB 61 KVSRYRGQEHCLHPKLGOSTRKRFIKWYNAMNEKRYEE 99

RESULT 3

M12B_RAT STANDARD; PRT; 100 AA.

AC 010747;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE MACROPHAGE INFLAMMATORY PROTEIN-2-BETA PRECURSOR (MIP2-BETA) (CINC-
 2-BETA).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RP SEQUENCE FROM N.A., AND SEQUENCE OF 33-100.

RC STRAIN=MISTAR;

RA Nakagawa H., Komorita N., Shibata F., Ikesue A., Konishi K.,

Fujioaka M., Kato H.;

RT "Identification of cytokine-induced neutrophil chemoattractants

(CINC), rat GRO/CINC-2 alpha and CINC-2 beta, produced by granulation

RT tissue in culture; purification, complete amino acid sequences and

RT characterization."

RL Biochem. J. 301:545-550(1994).
 RN [2]

RP SEQUENCE OF 33-52.

RC STRAIN=MISTAR;

RA MEDLINE-96183056; PubMed-8607872;

RT Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;

RT "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel

member of rat GRO/CINCS, is a predominant chemokine produced by

RT lipopolysaccharide-stimulated rat macrophages in culture."

RL Biochem. Biophys. Res. Commun. 220:945-948(1996).

-I- FUNCTION: MAY PLAY A ROLE IN INFLAMMATION AND EXERT ITS EFFECTS

ON ENDOTHELIAL CELLS IN AN AUTOCRINE FASHION.

-I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE

C-X-C) (CHEMOKINE CXC).

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EMBL: D21095; BAA04657.1; -

DR HSP; P10889; IMI2.

DR InterPro: IPR001811; Chemokine_IL8.

DR InterPro: IPR001089; Small_cytokine_CXC.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PRO0436; INTERLEUKIN8.

DR PRINTS: PRO0437; SMALLCYTCKXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.

DR CYTOKINE; Chemotaxis; Inflammatory response; Signal.

FT SIGNAL 1 32

FT CHAIN 33 100 MACROPHAGE INFLAMMATORY PROTEIN-

FT DISULFID 37 63 2-BETA.
 FT DISULFID 39 79 BY SIMILARITY.
 SO SEQUENCE 100 AA: 10989 MW: EB53ECFE30909D2 CRC64;

Query Match
 Best Local Similarity 35.1%; Score 143.5; DB 1; Length 100;
 Matches 34; Conservative 19; Mismatches 31; Indels 13; Gaps 3;

QY 8 APPVSRLLAALLLLALYARVDG-----KCKSRKPKRIYSYVKKLEKPKY 60
 DB 2 APP-TRRLNAALLLLALMATSHOPSQTVVARELRCKCLTLPVDFENIQSLVTPPG 60
 OY 61 PCEEKVITTKSVSRNGOEHCLHPKLOSTKRFK 97
 DB 61 PCHQTEVATLKD-----GQVCLNPQAPRLQKII 92

RESULT 4
 MIP2_MOUSE STANDARD; PRT; 100 AA.
 AC P10889;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MACROPHAGE INFLAMMATORY PROTEIN 2 PRECURSOR (MIP2).
 GN SCYB2 OR MIP2 OR MIP-2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90354792; PubMed=2201751;
 RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
 RA Febre M., Van Deventer S., Cerami A.;
 RT Cloning and characterization of cDNAs for murine macrophage
 RT inflammatory protein 2 and its human homologues.";
 RL J. Exp. Med. 172:911-919(1990).
 RN [2]
 RP SEQUENCE OF 28-59.
 RX MEDLINE=89098980; PubMed=2643119;
 RA Wolpe S.D., Sherry B., Juers D., Davatelis G., Yurt R.W., Cerami A.;
 RT Identification and characterization of macrophage inflammatory
 RT protein 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:612-616(1989).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98285558; PubMed=9622482;
 RA Shao W., Jerva L.F., West J., Lolits E., Schweitzer B.I.;
 RT Solution structure of murine macrophage inflammatory protein-2.";
 RL Biochemistry 37:8303-8313(1998).
 CC -1- FUNCTION: CHEMOTACTIC FOR HUMAN POLYMORPHONUCLEAR LEUCOCYTES BUT
 CC DOES NOT INDUCE CHEMOKINESIS OR AN OXIDATIVE BURST.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).
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 CC -----
 DR EMBL: X53798; CAA37807.1; -;
 DR PIR: JH0200; JH0200.
 DR PDB: 1MI2; 29-APR-98.
 DR MGD: MGI:1340094; SCYB2.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.

DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00436; INTERLEUKIN8.
 DR PRINTS: PR00437; SMALLCYTCKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 100 MACROPHAGE INFLAMMATORY PROTEIN 2.
 FT DISULFID 36 62
 FT DISULFID 38 78
 SO SEQUENCE 100 AA: 10621 MW: B9EFOA3218E92B5 CRC64;

Query Match
 Best Local Similarity 23.5%; Score 138; DB 1; Length 100;
 Matches 32; Conservative 21; Mismatches 31; Indels 12; Gaps 3;

QY 8 APPVSRLLAALLLLALYARVDG-----KCKSRKPKRIYSYVKKLEKPKY 61
 DB 2 APP-TRRLNAALLLLALMATSHOPSQTVVARELRCKCLTLPVDFENIQSLVTPPG 60
 OY 62 HCEEKVITTKSVSRNGOEHCLHPKLOSTKRFK 97
 DB 61 HCAQTEVATLKG-----GQVCLNPQAPRLQKII 91

RESULT 5
 GRO_CRIGR STANDARD; PRT; 101 AA.
 AC P09340;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GROWTH REGULATED PROTEIN PRECURSOR.
 GN SCYB1 OR GRO.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 NC NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041072; PubMed=2890161;
 RA Anisowicz A., Bartwell U., Sager R.;
 RT Constitutive overexpression of a growth-regulated gene in
 RT transformed Chinese hamster and human cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
 CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).
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 CC -----
 DR EMBL: J03560; AAA36985.1; -;
 DR PIR: B28414; B28414.
 DR HSSP: P10889; 1MI2.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00436; INTERLEUKIN8.
 DR PRINTS: PR00437; SMALLCYTCKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 101 POTENTIAL.
 FT DISULFID 37 63 GROWTH REGULATED PROTEIN.
 BY SIMILARITY.


```

DR 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG GAMMA PRECURSOR (GRO-GAMMA).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoshimura T., Modi W.S.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
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CC -----
CC EMBL: U95811; AAB93927.1; -
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; Small_cytokine_CXC.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00199; SCY.1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 68 GROWTH REGULATED PROTEIN HOMOLOG GAMMA.
FT DISULFID 39 65 BY SIMILARITY.
FT DISULFID 41 81 BY SIMILARITY.
SQ SEQUENCE 98 AA: 10393 MW: 94206897C21EDE9 CRC64:

Query Match 20.9%; Score 122.5; DB 1; Length 98;
Best Local Similarity 34.0%; Pred. No. 2,4e-06;
Matches 33; Conservative 16; Mismatches 35; Indels 13; Gaps 3;

OY 8 APPVSM-RLAALLLLLLALYTAARDG-----KCKGSRGKPKIRYSVYKLEMPK 59
Db 2 APAASAPRLRLAALLLLLLAAGRAAGAPVVELRCQCLQTLOGIHLKNISQKVTTP 61
OY 60 YPCEKKAVITTTKSVSRYSRRCQEHLPKLOSTKRFI 96
Db 62 GPHCDQTEVIADTKT-----GQEVCLNAPAAWVKIT 93

RESULT 10
GRO2_RABIT
AC ID GRO2_RABIT STANDARD; PRT; 104 AA.
AC P47854;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG PRECURSOR (GRO_HOMOLOG).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Schwartz D., Chaverri-Alameda L., Berliner J., Kirchgessner T.,
RA Quismonro D., Fang J., Tekamp-Olson P., Lusis J., Fogelman A.,
RA Terrio M.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLAYS A ROLE IN MONOCYTE ADHESION TO THE ENDOTHELIUM.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
```

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CC      -----
DR      EMBL; U12310; AAA20487.1; -.
DR      HSSP; P09341; IMGS.
DR      InterPro; IPR001811; Chemokine_IL8.
DR      InterPro; IPR001089; Small_cytokine_CXC.
DR      Pfam; PF00048; IL8; 1.
DR      PRINTS; PR00436; INTERLEUKIN8.
DR      PRINTS; PR00437; SMALLCYTCXC.
DR      SMART; SM00199; SCV; 1.
DR      PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW      Cytokine; Growth factor; Inflammatory response; Signal.
FT      SIGNAL             1           31
FT      CHAIN              32          104
FT      DISULFID            40           66
FT      DISULFID            42           82
FT      FTTF               BY SIMILARITY.
SQ      SEQUENCE          104 AA; 10900 MW; 10B9D07B65C77Fe7 CRC64;
Query Match                20.2%; Score 118.5; DB 1; Length 104;
Best local Similarity     32.6%; Pred. No. 6.8e-06;
Matches   31; Conservative 17; Mismatches 36; Indels 11; Gaps 2;
QY      8 APPYSRMRLAALALLLLLTALYTARVDG-----KCKSRKGPRIKRSVDVKLEMKPKYP 61
Db       5 ATAAPRFLRAALLLLLLLVAGRRAGAAPPVNELRQCGLDTLGSLHKLNQSVAVTTTPGP 64
QY      62 HCEKNMVIITTKSVSRIRNGDECHLPKIQTSKRTI 96
Db       65 HCDQTEVLASLKT-----GDVCLNPAPAYVKKII 94
RESULT 11
GROB_BOVIN STANDARD; PRT; 104 AA.
AC      046677;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      GROWTH REGULATED PROTEIN HOMOLOG BETA PRECURSOR (GRO-BETA).
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC      Bovidae; Bovinae; Bos.
NCBI_taxid=9913;
[1]
SEQUENCE FROM N.A.
RA      Yoshimura T., Modi W.S.;
RL      Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC      C-X-C) (CHEMOKINE CXC).
CC      -----
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U95813; AAB93929.1; -.
DR      InterPro; IPR001811; Chemokine_IL8.
DR      InterPro; IPR001089; Small_cytokine_CXC.
DR      Pfam; PF00048; IL8; 1.
DR      PRINTS; PR00436; INTERLEUKIN8.
DR      PRINTS; PR00437; SMALLCYTCXC.
DR      SMART; SM00199; SCV; 1.
```

DR SMART: SM00199; SCY: 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 104 GROWTH REGULATED PROTEIN HOMOLOG BETA.
 FT DISULFID 40 66 BY SIMILARITY.
 FT DISULFID 42 82
 FT DISULFID 42 82
 SQ SEQUENCE 104 AA; 10950 MW; 40ABCD6A64D67F7B CRC64;

Query Match 20.0%; Score 117.5; DB 1; Length 104;
 Best Local Similarity 31.6%; Pred. No. 8.7e-06;
 Matches 30; Conservative 18; Mismatches 36; Indels 11; Gaps 2;

QY 8 APPVSMKLLAALLLLALLLTARVDG-----KCKCRKGRKIRYSDVKLEMKPKYP 61
 5 ATAAAPRLTAAALLLLLVAGRRAGAPVYNELRCQCTQTGGHILKNINQSVKVTTPGP 64
 DB 62 HCEEKVITTKSVSRKRGCEHCLHKLKLOSTKRFI 96
 65 HCDQTEVIASLKT-----GQEVCLNPTAPVKKII 94

RESULT 12
 GRO_HUMAN STANDARD; PRT; 107 AA.
 AC P09341;
 ID 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GROWTH REGULATED PROTEIN PRECURSOR (MELANOMA GROWTH STIMULATORY
 DE ACTIVITY) (MGSA) (NEUTROPHIL-ACTIVATING PROTEIN 3) (NAP-3).
 GN SCYB1 OR GRO1 OR GROA OR GRO OR MGSA.
 OS Homo sapiens (Human).
 ON Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID:9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RA MEDLINE-88041072; PubMed-2890161;
 RA Anisowicz A., Bardwell L., Sager R.;
 RT "Constitutive overexpression of a growth-regulated gene in
 RT transformed Chinese hamster and human cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
 RN 12
 RP SEQUENCE FROM N.A.
 RA MEDLINE-88328991; PubMed-2970963;
 RA Richmond A., Balentien E., Thomas H.G., Flagg G., Barton D.E.,
 RA Spleess J., Bordon R., Francke U., Derynck R.;
 RT "Molecular characterization and chromosomal mapping of melanoma
 RT growth stimulatory activity, a growth factor structurally related to
 RT beta-thromboglobulin.";
 RL EMBO J. 7:2025-2033(1988).
 RN 13
 RP SEQUENCE FROM N.A.
 RA TISSUE-Blood;
 RC MEDLINE-91057157; PubMed-2129556;
 RA Baker N.E., Kucera G., Richmond A.;
 RT "Nucleotide sequence of the human melanoma growth stimulatory
 RT activity (MGSA) gene.";
 RL Nucleic Acids Res. 18:6453-6453(1990).
 RN 14
 RP SEQUENCE OF 35-65.
 RA MEDLINE-90217938; PubMed-2182761;
 RA Schroeder J.-M., Persson N.L.M., Christophers E.;
 RT "Lipopolysaccharide-stimulated human monocytes secrete, apart from
 RT neutrophil-activating peptide 1/interleukin 8, a second neutrophil-
 RT activating protein. NH2-terminal amino acid sequence identity with
 RT melanoma growth stimulatory activity.";
 RL J. Exp. Med. 171:1091-1100(1990).
 RN 15
 RP SEQUENCE OF 35-57.
 RX MEDLINE-89246368; PubMed-2655583;

RA Golds E.E., Mason P., Nyirkos P.;
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in
 RT human synovial cells and fibroblasts.";
 RL Biochem. J. 259:585-588(1989).
 RN 16
 RP POSSIBLE FUNCTION.
 RX MEDLINE-8935650; PubMed-2670560;
 RA Wen D., Rowland A., Derynck R.;
 RT "Expression and secretion of gro/MGSA by stimulated human endothelial
 RT cells.";
 RL EMBO J. 8:1761-1766(1989).
 RN 17
 RP STRUCTURE BY NMR.
 RX MEDLINE-93387459; PubMed-8397104;
 RA Fairbrother W.J., Reilly D., Colby T., Horuk R.;
 RT "1H assignment and secondary structure determination of human
 RT melanoma growth stimulating activity (MGSA) by NMR spectroscopy.";
 RL FEBS Lett. 330:302-306(1993).
 RN 18
 RP STRUCTURE BY NMR.
 RX MEDLINE-94376296; PubMed-8089846;
 RA Fairbrother W.J., Reilly D., Colby T., Hesselgeser J., Horuk R.;
 RT "The solution structure of melanoma growth stimulating activity.";
 RL J. Mol. Biol. 242:252-270(1994).
 RN 19
 RP STRUCTURE BY NMR.
 RX MEDLINE-95105175; PubMed-7806518;
 RA Kim K.S., Clark-Lewis I., Sykes B.D.;
 RT "Solution structure of GRO/melanoma growth stimulatory activity
 RT determined by 1H NMR spectroscopy.";
 RL J. Biol. Chem. 269:32909-32915(1994).
 CC -I- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. MAY PLAY A
 CC ROLE IN INFLAMMATION AND EXERTS ITS EFFECTS ON ENDOTHELIAL CELLS
 CC IN AN AUTOCRINE FASHION.
 CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
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 CC -----
 DR EMBL: J03561; AAA35933.1; -;
 DR EMBL: X12510; CA31027.1; -;
 DR EMBL: X54489; CA38361.1; -;
 DR PIR: A28414; A28414.
 DR PIR: S00983; S00983.
 DR PIR: S03976; S03976.
 DR PIR: S13669; S13669.
 DR PDB: 1MGS; 30-SEP-94.
 DR PDB: 1MSG; 31-MAR-95.
 DR MIM: 155730; -;
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00436; INTERLEUKIN8.
 DR PRINTS: PR00437; SMALLCYTOKCXC.
 DR SMART: SM00199; SCY: 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal; 3D-structure.
 FT SIGNAL 1 34
 FT CHAIN 35 107 GROWTH REGULATED PROTEIN.
 FT DISULFID 43 69
 FT DISULFID 45 85
 SQ SEQUENCE 107 AA; 11301 MW; 17048A6B4D765CA2 CRC64;

Query Match 20.0%; Score 117.5; DB 1; Length 107;

Db 65 HCDQTEVIASLKT-----GGQVCLNPTAPVKKII 94

RESULT 15

GRO_MOUSE STANDARD: PRT: 96 AA.

ID GRO_MOUSE P12850:

AC 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE GROWTH REGULATED PROTEIN PRECURSOR (PLATELET-DERIVED GROWTH FACTOR-INDUCIBLE PROTEIN KC) (SECRETORY PROTEIN N51).

GN SCYB1 OR GRO1 OR GRO OR MCSA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89139485; PubMed=2917992;

RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;

RT "The platelet-derived growth factor-inducible KC gene encodes a secretory protein related to platelet alpha-granule proteins.";

RL J. Biol. Chem. 264:4133-4137(1989).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=89078502; PubMed=2909392;

RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;

RT "Cloning and sequence of a secretory protein induced by growth factors in mouse fibroblasts.";

RL Exp. Cell Res. 180:266-275(1989).

RN [3]

RP SEQUENCE FROM N.A.

RX STRAIN=129/SV;

RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M., Conklyn M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;

RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE OF 1-10 FROM N.A.

RX TISSUE=Liver;

RA MEDLINE=96016008; PubMed=7561058;

RT Ohmori Y., Fukumoto S., Hamilton T.A.;

RT "Two structurally distinct kappa B sequence motifs cooperatively control LPS-induced KC gene transcription in mouse macrophages.";

RL J. Immunol. 155:3593-3600(1995).

CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).

CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXK).

CC -----

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CC -----

DR EMBL: J04596; AAA0131.1; -

DR EMBL: U20634; AAB03376.1; -

DR EMBL: U20527; AAB03376.1; JOINED.

DR EMBL: S79767; -; NOT_ANNOTATED_CDS.

DR PIR: A32954; A32954.

DR PIR: JH0081; JH0081.

DR HSSP: P09341; IMSH.

DR MGD: MGT:108068; Grol.

DR InterPro: IPR001811; Chemokine_IL8.

DR InterPro: IPR001089; Small_cytokine_CXC.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00436; INTERLEUKIN8.

DR PRINTS: PR00437; SMALLCYTKXC.

DR SMART; SMO0199; SCY, 1.

DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.

KW Cytokine; Growth factor; Inflammatory response; Signal.

FT SIGNAL 1 24 PROBABLE.

FT CHAIN 25 96 GROWTH REGULATED PROTEIN.

FT DISULFID 33 59 BY SIMILARITY.

FT DISULFID 35 75 BY SIMILARITY.

SO SEQUENCE 96 AA; 10254 MW; 4A52B5E5C38BA5C2 CRC64;

Query Match 18.9%; Score 111; DB 1; Length 96;

Best Local Similarity 30.8%; Pred. No. 3.9e-05;

Matches 28; Conservative 18; Mismatches 37; Indels 8; Gaps 2;

Qy 10 PSMRLLAALLLL---LALYARVDSKCKSRKGPRIKRSVDYKLEMPKYPHCEK 66

Db 3 PATSLICALLLLATSRATCAPIANERCCCLDTMAGIHKLNIOSLKVLPSPGHCTOT 62

Qy 67 MWITTSVSRVRYSGEHCILHPKLOSTKREIK 97

Db 63 EVIATLKN-----GRACLDPEAPLVOKIVQ 88

Search completed: January 29, 2002, 16:05:34

Job time: 120 sec

Wed Jan 30 09:49:26 2002

us-09-978-189-370.rsp

Page 10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 22.64 Seconds

(without alignments)
717.148 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 587
1 MSLLPRRAPVYSMRLAAL.....TKRFIKYNAWNEKRRVYE 111

Sequence: 1 MSLLPRRAPVYSMRLAAL.....TKRFIKYNAWNEKRRVYE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	587	100.0	111	4 Q9BTR1	Q9BTR1 homo sapien
2	582	99.1	111	4 Q9NS21	Q9NS21 homo sapien
3	506	86.2	99	11 Q9JHH7	Q9JHH7 brachydanio
4	371	57.1	100	13 Q9DFG4	Q9DFG4 gallus galli
5	322.5	54.9	98	13 Q9DGL8	Q9DGL8 gallus galli
6	143.5	24.4	101	11 Q9EP62	Q9EP62 rattus norv
7	128.5	21.9	98	6 Q28724	Q28724 cryctolagus
8	97.5	16.6	97	13 Q98TQ2	Q98TQ2 oncorhynch
9	93.5	15.9	126	11 Q99J60	Q99J60 mus musculu
10	89	15.2	113	11 Q9E015	Q9E015 mus musculu
11	87.5	14.9	111	11 Q99ME0	Q99ME0 rattus norv
12	86.5	14.7	104	13 Q73912	Q73912 gallus galli
13	86	14.7	93	13 Q9PTF8	Q9PTF8 brachydanio
14	83.5	14.2	101	6 Q9XSX5	Q9XSX5 felis silve
15	83.5	14.2	117	12 Q68398	Q68398 human cytom
16	76.5	13.0	59	6 Q62764	Q62764 equus cabal
17	76	12.9	98	11 Q9ERB1	Q9ERB1 mesocricetu
18	76	12.9	677	5 Q18209	Q18209 caenorhabdi
19	74.5	12.7	356	11 Q08889	Q08889 cricetus

20	74	12.6	394	5 Q44635	Q44635 caenorhabdi
21	72.5	12.4	131	13 Q9PV19	Q9PV19 harpador sp
22	72.5	12.4	356	11 Q88464	Q88464 mus musculu
23	72.5	12.4	356	11 Q9JLK2	Q9JLK2 mus musculu
24	71.5	12.2	102	4 Q9C077	Q9C077 homo sapien
25	71.5	12.2	1417	5 Q9VSE1	Q9VSE1 drosophila
26	71	12.1	475	12 Q9QD14	Q9QD14 pleione vir
27	71	12.1	1270	5 Q23658	Q23658 caenorhabdi
28	70.5	12.0	356	4 Q75036	Q75036 homo sapien
29	70	11.9	101	13 Q93442	Q93442 lampetra fl
30	69	11.8	599	4 Q9P0M8	Q9P0M8 homo sapien
31	68.5	11.7	97	11 Q92318	Q92318 cavia porce
32	68	11.6	149	5 Q22745	Q22745 caenorhabdi
33	68	11.6	204	10 Q9M5N2	Q9M5N2 aegilops ve
34	68	11.6	581	1 Q9H0Y4	Q9H0Y4 halobacteri
35	68	11.6	751	11 P70535	P70535 rattus norv
36	67	11.4	647	4 Q94815	Q94815 homo sapien
37	67	11.4	648	4 Q9P38	Q9P38 homo sapien
38	66.5	11.3	86	11 Q9QX28	Q9QX28 mus musculu
39	66.5	11.3	272	5 Q9VEM6	Q9VEM6 drosophila
40	66.5	11.3	346	2 P70801	P70801 anabaena va
41	66.5	11.3	397	2 Q65659	Q65659 aquifex aeo
42	66.5	11.3	1632	5 Q9NDH2	Q9NDH2 caenorhabdi
43	66.5	11.3	3228	5 Q93593	Q93593 caenorhabdi
44	66	11.2	346	4 Q14877	Q14877 homo sapien
45	66	11.2	6815	5 Q91704	Q91704 drosophila

ALIGNMENTS

RESULT 1
Q9BTR1 PRELIMINARY: PRT: 111 AA.
AC Q9BTR1:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SMALL INDICIBLE CYTOKINE SUBFAMILY B (CYS-X-CYS), MEMBER 14 (BRK).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREATIC ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL, BC003513; AA003513.1;
SQ SEQUENCE 111 AA: 13077 MW: C9A18B2A/8CACE74 CRC64;

Query Match 100.0%; Score 587; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.7e-58;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLLPRRAPVYSMRLAALLLLLALTYARYDSKCKSRGPKIRYSDVKLEMPKY 60
DB 1 MSLLPRRAPVYSMRLAALLLLLALTYARYDSKCKSRGPKIRYSDVKLEMPKY 60
QY 61 PRCCEKMWIITTKSVSRGGECHLPHKLOSTKRIKYNAMNEKRRVYE 111
DB 61 PRCCEKMWIITTKSVSRGGECHLPHKLOSTKRIKYNAMNEKRRVYE 111
ID Q9NS21
AC Q9NS21; PRELIMINARY: PRT: 111 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHEMOKINE MIP-2 GAMMA.

GN MIP-2 GAMMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Yuan Z., Cao X.;
RT "A novel chemokine gene, MIP-2 gamma,"
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF106911; AAF78449.1; -
DR InterPro: IPR001811; Chemokine_IL8.
DR SMART: SM00199; SCY: 1.
SQ SEQUENCE 111 AA; 13126 MW; C9A18B3178CACE74 CRC64;

Query Match 99.1%; Score 582; DB 4; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.4e-57;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSLLPRAPVSMRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKY 60
Db 1 MSLLPRAPVSMRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKY 60

QY 61 PCEEEKVITTTKSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 111
Db 61 PCEEEKVITTTKSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 111

RESULT 3
Q9JHH7 PRELIMINARY; PRT; 99 AA.
AC Q9JHH7;
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 17, Last annotation update)
DE B CELL AND MONOCYTE-ACTIVATING CHEMOKINE PRECURSOR (BRAIN CDNA, CLONE
NMBC-6413), SIMILAR TO MUS MUSCULUS KIDNEY-EXPRESSED CHEMOKINE CXC
DE (KEC) MRNA (KRC) (1200006123RIK PROTEIN).
GN SCYB14 OR BMAC OR 1200006123RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALE/CBYJ;
RA Sleeman M.A., Fraser J.K., Murison J.G., Kelly S.L., Prestidge R.,
RA Watson J.D., Kumble K.D.;
RT "B cell and monocyte-activating chemokine (BMAC), a novel non-ELR
RT alpha chemokine."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Osaka N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.;
RT "Isolation of full-length cDNA clones from mouse brain cDNA library
RT made by oligo-capping method."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD, AND LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojofori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Caslavac T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kocich H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fleischner C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AF144754; AAF6694.1; -
DR EMBL: AB041614; BAA95097.1; -
DR EMBL: AK014351; BAB29292.1; -
DR EMBL: AK004615; BAB23411.1; -
DR MGD: MGI:1888514; Scybl4.
DR MGD: MGI:1915056; 1200006123RIK.
DR InterPro: IPR001811; Chemokine_IL8.
DR SMART: SM00199; SCY: 1.
KM Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 99 B CELL AND MONOCYTE-ACTIVATING
FT CHEMOKINE.
SQ SEQUENCE 99 AA; 11716 MW; 9735291FF7F46D6 CRC64;

Query Match 86.2%; Score 506; DB 11; Length 99;
Best Local Similarity 94.9%; Pred. No. 6.3e-49;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 13 MRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKYPPHCEEKVITTT 72
Db 1 MRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKYPPHCEEKVITTT 72

QY 73 KSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 111
Db 61 KSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 99

RESULT 4
Q9DFG4 PRELIMINARY; PRT; 100 AA.
AC Q9DFG4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CXC-TYPE CHEMOKINE.
GN SCYB4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
ON NCBI_TaxID=7955;
RX [1]
RP SEQUENCE FROM N.A.
RC PubMed=11025222;
RA Long Q., Quint E., Lin S., Ekker M.;
RT "The zebrafish scyba gene encodes a novel CXC-type chemokine with
RT distinctive expression patterns in the vestibulo-acoustic system
RT during embryogenesis."
RL Mech. Dev. 97:185-186(2000).
DR EMBL: AF279919; AAG09819.1; -
SQ SEQUENCE 100 AA; 12016 MW; 274BE255A74F98B5 CRC64;

Query Match 57.1%; Score 335; DB 13; Length 100;
Best Local Similarity 54.6%; Pred. No. 7.2e-30;
Matches 53; Conservative 25; Mismatches 19; Indels 0; Gaps 0;

QY 14 RLTAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKYPPHCEEKVITTT 73
Db 3 RCTAALLFLVAVSLNTEAKCKCTKPKIRITDVQKLEIKPKHPCQEKMFVME 62

QY 74 SVSRVGOEHCHPKLOSTRKFIKYNAMNKKRYVE 110
 Db 63 NVSRFKGQETCLHPRLDSTRNLVAKWFKWKDRTTFF 99

RESULT 5

Q9DGL8 PRELIMINARY; PRT; 98 AA.

AC Q9DGL8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE JUN-SUPPRESSED CHEMOKINE.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.

NCBI_TaxID=9031;

Sequence from N.A.

Tissue=FIBROBLAST;

Harli M., Bister K.;

Suppression of genes in jun-transformed avian fibroblasts.

Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

EMBL: AF285876; AAC00529.1; 30D88E540ADD35B CRC64;

Query Match 54.9%; Score 322.5; DB 13; Length 98;
 Best Local Similarity 60.0%; Pred. No. 1,7e-28;
 Matches 60; Conservative 19; Mismatches 18; Indels 3; Gaps 2;

QY 13 MRLAALALLLLALYARYDGSCKSCSRKGPRIYSDVKLEKPKYPHCEKMYITTT 72
 Db 1 MKLTLALLLVYAMCLASABGVKCKSRKGPRIYSDVKLEKPKYPHCEKMYITTT 60

QY 73 KVSRYNG-QECLHPKLOSTRKFIKYNAMNKKRYVE 111
 Db 61 -WTKVRGEQOHCINPRONTVLLKMYRWKKEGRVYEE 98

RESULT 6
 Q9EP62 PRELIMINARY; PRT; 101 AA.

AC Q9EP62;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE CINC-2 ALPHA PRECURSOR.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

Sequence from N.A.

Strain=Wistar; Tissue=PERITONEAL CAVITY;

Medline=98236997; PubMed=9576061;

Shibata F., Konishi K., Nakagawa H.;

Gene structure, cDNA cloning, and expression of rat cytokine-induced neutrophil chemoattractant 2 (GRO/CINC-2) gene.

Cytokine 10;165-174(1998).

EMBL: D87927; BAB12280.1; -

EMBL: D87926; BAB12279.1; -

InterPro: IPR001811; Chemokine_IL8.

InterPro: IPR001089; Small_cytokine_CXC.

Pfam: PF00048; IL8; 1
 PRINTS: PR00437; SMALLCYTKCXC.
 SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR SIGNAL.
 FT CHAIN 1 32 POTENTIAL.
 33 101 CINC-2 ALPHA.

SQ SEQUENCE 101 AA; 11109 MW; D949D5712FE30909 CRC64;

Query Match 24.4%; Score 143.5; DB 11; Length 101;
 Best Local Similarity 35.1%; Pred. No. 1,6e-08;
 Matches 34; Conservative 19; Mismatches 31; Indels 13; Gaps 3;

QY 8 APPVSMRLAALALLLLALYARYDGS-----KCKSCSRKGPRIYSDVKLEKPKYP 60
 Db 2 APP-TRRLNLAALALLLLALYARYDGS-----KCKSCSRKGPRIYSDVKLEKPKYP 60

QY 61 PHCEKMYITTTKVSRYNGQEHCHPKLOSTRKFIK 97
 Db 61 PHCTQTEVIATLKD-----GQEVCLNPOAPRLQIKI 92

RESULT 7

Q28724 PRELIMINARY; PRT; 108 AA.

AC Q28724;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE GRO (PERMEABILITY FACTOR 2).

OS RPF2.

OC Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NCBI_TaxID=9986;

Sequence from N.A.

Strain=NEW ZEALAND WHITE;

Yoshimura T., Modi W.S.;

Isolation of novel GRO genes, and a phylogenetic analysis of the CXC chemokine subfamily in mammals.

Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

Sequence of 43-108 from N.A.

Strain=NEW ZEALAND WHITE;

Medline=95129889; PubMed=7828903;

Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,

Marlin T.R.;

"Cloning of two rabbit GRO homologues and their expression in alveolar macrophages."

Gene 151;337-338(1994).

EMBL: U95808; AAB93924.1; -

EMBL: I28933; AAB66975.1; -

HSP; P19875; IONK.

InterPro: IPR001811; Chemokine_IL8.

InterPro: IPR001089; Small_cytokine_CXC.

Pfam: PF00048; IL8; 1.

PRINTS: PR00437; SMALLCYTKCXC.

SMART: SM00199; SCY; 1.

PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR SIGNAL.
 FT CHAIN 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;

Query Match 21.9%; Score 128.5; DB 6; Length 108;
 Best Local Similarity 33.3%; Pred. No. 7,9e-07;

Matches 32; Conservative 15; Mismatches 38; Indels 11; Gaps 2;

QY 8 APPVSMRLAALALLLLALYARYDGS-----KCKSCSRKGPRIYSDVKLEKPKYP 61
 Db 9 AAPSGRFLRTAMLLLLLLAASRAAGAAALTELKCGCQLYQVGHILKSLQKLVLSRPG 68

QY 62 HCEKMYITTTKVSRYNGQEHCHPKLOSTRKFIK 97
 Db 69 HCAQTEVIATLKS-----GQEVCLNPOAPRWKFLQ 99

RESULT 8
 Q98T02 PRELIMINARY; PRT; 97 AA.

Q98T02

AC 099ME0;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CXC CHEMOKINE RTCK1.
 GN RTCK1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fu W., Gong S., Chen W.;
 RT "Cloning and Characterization of a Novel Gene Coding the Homologous
 RT Gene to RTCK1."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF349115; AAK30166.1;
 SQ SEQUENCE 111 AA; 12159 MW; 8230226BC7C60A55 CRC64;

Query Match 14.9%; Score 87.5; DB 11; Length 111;
 Best Local Similarity 23.9%; Pred. No. 0.03;
 Matches 22; Conservative 22; Mismatches 37; Indels 11; Gaps 2;
 QY 12 SMRLAALLLLALTYARVDS-----KCKSRKPKIRYSDVKLEMKPKYHCEE 65
 DB 19 NLQVLSLLVLAALVPLANGKPDNNEPTELRCCTNLISLISISRVNFRGACHDN 78
 QY 66 KMWITTKSVSRYGQEHCLPKLQSTKRFRK 97
 DB 79 VEVATLTKN-----GKEVCLDPTAPMIRKIKY 105

RESULT 12
 ID 073912 PRELIMINARY; PRT; 104 AA.
 AC 073912;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE K60 PROTEIN PRECURSOR (CXC CHEMOKINE K60).
 GN K60.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-MACROPHAGE LIKE;
 RL Slick C.;
 RN Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20170941; PubMed=10704244;
 RA Slick C., Schneider K., Staeheli P., Weinling K.C.;
 RT "Novel chicken CXC and CC chemokines."
 RL Cytokine 12:181-186(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hughes S.M., Bumstead N.;
 RT "Mapping of a second ELR CXC chemokine to chicken chromosome four."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y14971; CAA75212.1;
 DR EMBL; AF277660; AAF6485.1;
 DR HSSP; P02775; ITVX.
 DR Interpro; IPR001811; Chemokine_IL8.
 DR Interpro; IPR001089; Small_cytokine_CXC.
 DR Pfam; PF00048; IL8; 1
 DR PRINTS; PRO0437; SMALLCYTKKCX.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Signal.

FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 104 K60 PROTEIN.
 SQ SEQUENCE 104 AA; 11199 MW; 83725AB91F18B3D CRC64;

Query Match 14.7%; Score 86.5; DB 13; Length 104;
 Best Local Similarity 28.3%; Pred. No. 0.036;
 Matches 25; Conservative 15; Mismatches 38; Indels 13; Gaps 3;
 QY 14 RLNALALLLLALTYARVDS-----KCKSRKPK-IRSDVKLEMKPKYHCEE 65
 DB 4 KAVAAVALLLISMAAGKAGAAQARSALTELCQCIETHSKPIHPKIFQNVNLTPSGPCKN 63
 QY 66 KMWITTKSVSRYGQEHCLPKLQSTKRFRK 97
 DB 64 VEVATLTKD-----GKEVCLDPTAPMIRKIKY 90

RESULT 13
 ID 09PTF8 PRELIMINARY; PRT; 93 AA.
 AC 09PTF8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CC CHEMOKINE CCL1.
 GN CCL1.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tseng S., Rollins B.J.;
 RT "Chemokines and chemokine receptors in zebrafish."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF201450; AAF17560.1;
 DR Interpro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 SQ SEQUENCE 93 AA; 10776 MW; 17C9B5309903ED7 CRC64;

Query Match 14.7%; Score 86; DB 13; Length 93;
 Best Local Similarity 29.4%; Pred. No. 0.037;
 Matches 25; Conservative 15; Mismatches 27; Indels 18; Gaps 3;

QY 22 LLLALLTY-----ARYDSKCKSKRKPRIYSDVKLEMKPKYHCEEKVIIT 72
 DB 8 LLLVCFITILLDNKGAAIPTCISLVLRIRPRVLRVRYEQDTSGHCIFKLLIL-- 65
 QY 73 KSVSRYRGQEHCLPKLQSTKRFRK 97
 DB 66 ----HFKGKKICAHPKLE--RFLK 83

RESULT 14
 ID 09XSX5 PRELIMINARY; PRT; 101 AA.
 AC 09XSX5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE INTERLEUKIN-8.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straubinger A.F., Straubinger R.K.;
 RT "Feline interleukin-8 mRNA."

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF158598; AAD40323.1; .
 DR HSSP: P10145; 1IKM.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR Pfam: PF000048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR SEQUENCE 101 AA; 11165 MW; 690D97F13EF79170 CRC64;

Query Match 14.2%; Score 83.5; DB 6; Length 101;
 Best Local Similarity 28.0%; Pred. No. 0.076; Indels 17; Gaps 5;
 Matches 28; Conservative 19; Mismatches 36;

QY 15 LLAALLLL--ALTARVDS--KCCSRK-----GPKIRYSDVKLEMKPKYPHCEEK 66
 DB 9 LLAFFMLSAALCEAAVLSRISSELRCCCTKHTSTPNPKL----IKELTVIDSGPHCENS 64
 QY 67 MVIITKSVSRVGRGHECHLPKIQSTKRFIKWYNNNEKR 106
 DB 65 EII-----KLVNGKEVCIDPKQKQWQKXVEIFLKKAEKQ 99

RESULT 15
 ID Q68398 PRELIMINARY; PRT; 117 AA.
 AC Q68398;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)
 DE ORF UL146.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOLEDO;
 RX MEDLINE=96099416; PubMed=8523595;
 RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
 RT "Human cytomegalovirus clinical isolates carry at least 19 genes not
 found in laboratory strains."
 RL J. Virol. 70:78-83(1996).
 DR EMBL: U33331; AAA85885.1; .
 SQ SEQUENCE 117 AA; 13658 MW; E37A805502A9A0A4 CRC64;

Query Match 14.2%; Score 83.5; DB 12; Length 117;
 Best Local Similarity 27.5%; Pred. No. 0.088;
 Matches 30; Conservative 15; Mismatches 33; Indels 31; Gaps 6;

QY 13 MRLAALLLLLALTYARYDGS--KCKC-SRGP--KIRYSDVKLEMKPKYPHCEEK 67
 DB 1 MRLIFGALLIFLAVYVYENGTELRCCLHRKWPKNKILLGNV-WLHRDPGPGCDK-- 57
 QY 68 VIITKSVSRVGRGHECHLPK-----LQSTKRFIKWYNNNEKR 106
 DB 58 -----NEHLLYPDGRRKPPGPGVCLSPDHLFSKWLDKHNDNR 93

Search completed: January 29, 2002, 16:05:16
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AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 108123)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 108123)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (21-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 4 (bases 1 to 108123)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Jun 21, 2001 this sequence version replaced gi:9256720.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40.99.5% of Sequence;
 Estimated Total Number of Errors is 0.2.
 STS Content:
 SHGC-130469 G59717.
 Location/Qualifiers
 source 1. 108123
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTC-321K16"
 BASE COUNT 27996 a 23419 c 26053 g 30655 t
 ORIGIN
 Query Match 70.0%; Score 1179.2; DB 9; Length 108123;
 Best Local Similarity 99.7%; Pired. No. 1.5e-217;
 Matches 1192; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 962 gctgcacaggctcctcctggtctatggtccggtcacagcctcagtgtaactccacagtg 1021
 |||||||
 Db 17100 GCTGCCAGGGCTCTCCTGGGGCTTATGGCGGTACAGCCCTCATGTGAGCTCCACAGTGG 17041
 QY 1022 cccctgtacggcgcaagcaggaagcaggtctctctgcatctgtctctctggaactcaag 1081
 |||||||
 Db 17040 CCCCTGTAGCGGGGCAACAGAGAGAGTCTGTGATCTGTCTGTGAGAACTCAAG 16981
 QY 1082 ttgtgtccagaataatgctctatcccccttggttaatttttcacacccctagaa 1141
 |||||||
 Db 16980 TTTGGTCCAGAAAAATGCTCTTATTCCTCCCTGGTTAATTTTACACACCTTAGAA 16921
 QY 1142 acattccaagatcctgtgatggtgagacaatgatcccttaagaagtggtggtctt 1201
 |||||||
 Db 16920 ACATTTCAGATCTCTGTGATGCGCAGCAATATGCTTAAAGAGGTGGGCTCTT 16861
 QY 1202 cccaactgtagattcttgaaaggttcacaggttcaatattatgcttcagaagcatgt 1261
 |||||||
 Db 16860 CCCAAGCTGAGGATTTTGAAAGGTTTCACAGTTCAATATTTAATGCTTCAGAAAGCATGT 16801
 QY 1262 gagggtcccaacactgtcagcaaaaaacttgaggaaacttaaatatataatgatac 1321
 |||||||
 Db 16800 GAGGTTCCCAACACTGTGAGCAAAAACCTTAGGAGAAAACTTAAATATATGATACAT 16741
 QY 1322 ggcacatacacagctacagacacacatctgttgcaagggaagaaacttcacaaatg 1381
 |||||||
 Db 16740 GCGCAATACACAGCTACAGACACATCTGTGCAAGGGAACCTTCAACAGATGT 16681
 QY 1382 tcttccctcacacaagaacatgacagtaactaaagcaatatttgatltcccatg 1441
 |||||||
 Db 16680 TCTTTCCCTCACACACAGAACATGACATTAAGCAATATATTTGATTCCTCCATG 16621
 QY 1442 taattctcaatgtaaacagtgagctctcttgcgaagtaagatgacatgcgacct 1501
 |||||||
 Db 16620 TAATTTCTAAAGTTAAACAGTGCGCTCTTCTTGAAAGCTAACATACCATGCGCCT 16561
 QY 1502 ttcctcgtacataccttaagaagcgcctccacacacatgcgccccagatatagc 1561
 |||||||
 Db 16560 TTCCCTGTACATATACCTTAAAGAGCCCTCCACACATGCCCCCAGTATATGCC 16501
 QY 1562 gcaatgtactcgtgtatataatgcatgacatgcaaaacatagcatgtatgag 1621
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 Db 16500 GCATTGTACTGCTGTATATATGCTATGATGTCACAAACCATATACATTTGATGAG 16441
 QY 1622 gttcatattcttcttaagatgaaagtaataatatattgaaatgaaatgaaatgaa 1677
 |||||||
 Db 16440 GTTTCATATTCTTTTACATGGAAGATATATATTTTGAATGTACCAAAA 16385
 |||||||

RESULT 4
 AC005738/c
 LOCUS Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete
 DEFINITION
 ACCESSION AC005738 AC004619 L81405 L81406 L81678 L81679 L81680 L81860 L81861
 L81862 AC001042 AC001043 AC001044 AC001045
 VERSION AC005738.1 GI:3687213
 KEYWORDS
 SOURCE HTG
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 134506)
 AUTHORS Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M.,
 Kader, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M.,
 Rojowski, H., Subramanian, S., and Martin, C.H.
 TITLE Sequencing of human chromosome 5
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 134506)
 AUTHORS Riche, D.O.
 TITLE Large Scale Sequence Analysis and Annotation with the Sequence
 Comparison Analysis (SCAN) System
 JOURNAL Unpublished

```

REFERENCE      3 (bases 1 to 134506)
AUTHORS        Kimmery,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
                Kader,K., Miguel,T., Miller,C., Piltuck,S., Pollard,M.,
                Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE          Direct Submission
JOURNAL        Submitted (01-OCT-1998) Human Genome Center, DOE Joint Genome
                Institute, Lawrence Berkeley National Laboratory, MS 74-157,
                Berkeley, CA 94720, U.S.A.
REFERENCE      4 (bases 1 to 134506)
AUTHORS        Ricke,D.O.
TITLE          Direct Submission
JOURNAL        Submitted (13-OCT-1998) Los Alamos National Laboratory, DOE Joint
                Genome Institute, T443, HRL-1, LS-3, MS M888, Los Alamos, NM 87545,
                USA
REFERENCE      5 (bases 1 to 134506)
AUTHORS        Ricke,D.O.
TITLE          Direct Submission
JOURNAL        Submitted (20-OCT-1998) Los Alamos National Laboratory, DOE Joint
                Genome Institute, T443, HRL-1, LS-3, MS M888, Los Alamos, NM 87545,
                USA

COMMENT        Sequence submitted by:
                DOE Joint Genome Institute.
FEATURES
source         1.134506
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                +db_xref="taxon:9606"
                +map="5p"
                +chromosome="5"
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                +db_xref="taxon:9606"
                +chromosome="5"
                +map="5p"
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                repeat_region complement(3940..4205)
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                complement(5036..5148)
                +rpt_family="MIR"
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                repeat_region 9745..10340
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                +db_xref="taxon:9606"
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QY 542 gagacttgcgaagagcttgcagatlaaaaaaagaaaaaagaaaaaagaaaaa 601
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Db 111063 GAGACTTGTGCAAGGACTTTCGAGATT--AAAAAAGGAAAAAAGAAAAAAGAAAAA 111006

QY 602 aaaaaaagcccttcttcttcacagcagaacacaaatataatattgtatgaa 661
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Db 111005 AAAAAAAGGCTTCTTCTTCACAGGCAATGAAACACAAATTAATATTGTTATGAA 110946

QY 662 gcaactttacaaagcagcttttcaatttatactgctgcgaagagcttcagat 721
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Db 110945 GCACTTTTACCAAGGCTTTCATATTATTAAGCTGCTGCGAAGGCTCCAGAT 110886

QY 722 gggagaccatctctctgtgtccagactcaccagcagctgtcttttcaaaaaag 781
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Db 110885 GGGAGACCCATCTCTGTGCTCCAGACTCATCACAGGCTGCTTTTATCAAAAGGG 110826

QY 782 gaaacatagctcttctttaaabaatgcttttggatattgtccatacgtcactat 841
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Db 110825 GAAACATCATGCTCTTCTTTTAAAAAATGCTTTTGTATTTGTCATACGTCACCTAT 110766

QY 842 acatctgagctttaaagccggaaggaacatgagctgtgtggaacatttcatg 901
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Db 110765 ACATCTGAGCTTTTAAGCGCCGCGGAGGAACATGACCTTGCGACACATTTTCATGCG 110706

QY 902 agtltgtccatctcactagcttggaaagcttcgacttagaggttcctgtgcctcggaca 961
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Db 110705 AGTGTGCTCATTCCTAGCTTGGGAAGCTTCGCTTAGAGTCTCGCGCTCGGACCA 110646

QY 962 gctgcgaaggtctctctggactatgagcggtacagagctcagttgtgactcccaatgg 1021
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Db 110645 GCTGCAGAGGCTCTCCGTGGGCTTATGCGCGTACAGCCCTCACTGTGATCCACAGTGG 110586

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QY 1022 cccctgtgacggggaagcagagcaggtctctctgcatctgtctcgaagaaactaag 1081
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QY 1082 ttgtgttcgaagaaatgtgtcttcatctcccccgtgttaattttacacaccttaaggaa 1141
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Db 110525 TTGTGTGTCAGAAAAATGTGCTTCATTCGCCCTGTGTAAATTTTACACACCCCTAGGAA 110466

QY 1142 acatttcaagaatctctgtatgtgaggaanaatgatacctttaaagaagtgtgggtctt 1201
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Db 110465 ACATTTTCCAAAGATCCTGTATGCGCAGACAAATGATCCTTAAAGAGGTGTGGGCTCTTT 110406

QY 1202 cccaactgaggaattctttaaaggttcacaggttcaataattaaagcttcagaagcagt 1261
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Db 110405 CCCAAGCTGAGATTTCTTCAAAAGTTTCACAGGTTCAATATTAAATGCTTCAGAACACATGT 110346

QY 1262 gaggttcccaacacgttcagcaaaaaaccttaaggaaaaacttaaaatatatgatacat 1321
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Db 110345 GAGGTTCACCAACACTGTACAGCAAAACCTTACAGCAAAACCTTAAATATATGATACAT 110286

QY 1322 ggcgaataacacagctacagacacacattctgttgcagaaggaacaccttaagaagtgt 1381
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Db 110285 GCGCAATACACAGCTACAGACACACATCTGTGACAAAGGAAACCTTCAAAAGCATGT 110226

QY 1382 tcttccctcacacacagaaacatgcaatgactaaagacataattgtgaltcccaatg 1441
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QY 1442 taatttcaaatgttaaacagtgagctcctcttcgaaagctaaagtacatgagccct 1501
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QY 1502 tctctctgacatataccctttaaagaagcccccctcacacactgtcccccagatatgccc 1561
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QY 1562 gcaatgactgctgtgtatcgtatgacatgacatgtaagaacatagatgcatgacag 1621
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RESULT 5
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LOCUS Homo sapiens chromosome 5 clone XBP1-380H11, WORKING DRAFT
DEFINITION AC011428
ACCESSION AC011428
VERSION AC011428.3 GI:11178060
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 79970)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
PUBLISHED 2 (bases 1 to 79970)
DOE Joint Genome Institute.
REFERENCE 2 (bases 1 to 79970)
DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 15, 2000 this sequence version replaced g1:6604400.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information

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Center Project Name: 1189149, H122
Center Clone name: XXp1-380H11

Summary Statistics

Consensus quality: 76910 bases at least Q40
Consensus quality: 78432 bases at least Q30
Consensus quality: 78894 bases at least Q20
Estimated insert size: 72000; pulse field gel estimation
Estimated insert size: 76700; sum-of-coverage estimation
Quality coverage: 7.19 in Q20 bases; pulse field gel estimation
Quality coverage: 6.49 in Q20 bases; sum-of-coverage estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES

source

1. 79970
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/db_xref="taxon:9606"
/chromosome="5"
/clone="XXp1-380H11"

BASE COUNT 20846 a 18934 c 18691 g 21162 t 337 others

ORIGIN

Query Match

Best Local Similarity 69.8%; Score 1175.6; DB 2; Length 79970;
Matches 1190; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

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18584 GAGACTTGTGCAAGAGCACTTGCAGAT--AAAAAATAAAAAAATAAAAAAATAAAAAA 18527
602 aaaaaaataaaagccttctctcacaagcagcacaacaatatatctgtatgaa 661
18526 AAAAAAATAAAACCTCTTCTCTCAGAGCATTAAGCAACAATATATATTTGTTATGAA 18467
662 gacatttaccagaagtgatgttaccattatagtcgctgcaagaaggtccagat 721
18466 GCACCTTTTACCAAGCGTATGTTTACATTTTATAGCTGCGGCAAGGCTTCCAGAT 18407
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842 acatctgactatataagcccgaggaagaacaatagctgtgagacattcatcag 901
18286 ACATCTGACTTATATAGGCGCGGAGAGACATAGCTTGTGTGACACATTTTATTTGC 18227
902 agtctgctcactctcagcttggaagcttcogcttagagtcctgctcctgagca 961
18226 AGATATGCTTCATTTCTACTGCTGGGAAAGCTTCGGCTTAAGAGTCCGCGCTCGGACA 18167
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1022 cccctgtagccggaggaacagagcaggtctctctgcatctgctctcgaagaaactcaag 1081
18106 CCCCTGTACCCGGGCAAGAGGAGGAGGCTCTCTGCAATCTGTTCTTGAGGAACCTCAG 18047
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1202 ccbaaccctgagatcttctgaaaggttcaaggttcaatattatattagcttcaagacatg 1261
17926 CCCAACCTGAGGATTTGTGAAGGTTCAAGGTTCAATATTTAATGCTTCAGAACATGT 17867
1262 gaggttcccaaacactgtcagcaaaaaccttagagagaacttaaaatataatgatacat 1321
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17806 GCGCATACACAGCTACAGACACACATTTCTGTGCAAGGAAAACTTCAAGCATGTT 17747
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17686 TAAATCTTCAATGTAAACAGTGCAGTCTCTTGTGAAAGCTAAGATACCATGCGCCCT 17627
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1562 gcatgtgactctgtgtatattgctatgcatgcatgctgcaaaacattgcatgcatgag 1621
17566 GCAATGTACTGTGTTATATGCTATGTACATGTGCAAAAACCATTCACATGTGATGAG 17507
1622 gtctcatattcttcttcaagatgaaagtaataatatattgaaatglaaaaaa 1677
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DEFINITION 26 unordered pieces.
ACCESSION AC009017
VERSION AC009017.4 GI:13699469
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 159420)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159420)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Apr 20, 2001 this sequence version replaced gi:1178048.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI

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 LOCUS Homo sapiens chromosome 5 clone Xxp1-766F5, WORKING DRAFT SEQUENCE,
 DEFINITION 11 ordered pieces.
 AC063981
 VERSION AC063981.2 GI:9964804
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 81811)
 DOE Joint Genome Institute.
 Title
 JOURNAL Sequencing of Human Chromosome 5
 REFERENCE Unpublished
 AUTHORS 2 (bases 1 to 81811)
 TITLE DOE Joint Genome Institute.
 JOURNAL Direct Submission
 COMMENT Submitted (22-APR-2000) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Sep 2, 2000 this sequence version replaced gi:7636394.
 -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: http://www.jgi.doe.gov

 Project Information
 Center Project Name: 1189125, H199
 Center clone name: Xxp1-766F5

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 Consensus quality: 74154 bases at least Q40
 Consensus quality: 79224 bases at least Q30
 Consensus quality: 80246 bases at least Q20
 Estimated insert size: 76000; pulse field gel estimation
 Estimated insert size: 81361; sum-of-coverage estimation
 Quality coverage: 5.65 in Q20 bases; pulse field gel estimation
 Quality coverage: 5.28 in Q20 bases; sum-of-coverage estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 3978: contig of 3978 bp in length
 * 3979 4078: gap of unknown length
 * 4079 42436: contig of 38358 bp in length

* 42437 42536: gap of unknown length
 * 42537 44222: contig of 1686 bp in length
 * 44223 44322: gap of unknown length
 * 44323 50495: contig of 6173 bp in length
 * 50496 50595: gap of unknown length
 * 50596 51958: contig of 1363 bp in length
 * 51959 52058: gap of unknown length
 * 52059 55493: contig of 3435 bp in length
 * 55494 55593: gap of unknown length
 * 55594 65183: contig of 9590 bp in length
 * 65184 65283: gap of unknown length
 * 65284 69297: contig of 4014 bp in length
 * 69298 69397: gap of unknown length
 * 69398 71766: contig of 2369 bp in length
 * 71767 71866: gap of unknown length
 * 71867 80791: contig of 8925 bp in length
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /chromosome="5"
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 Best Local Similarity 99.4%; Pred. No. 1.5e-214;
 Matches 1189; Conservative 0; Mismatches 4; Indels 3; Gaps 2;
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 QY 542 gagactgtgcaagagacttgcagatcaaaaaaagaaaaaagaaaaaagaaaaa 601
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 Db 15985 GAGACTGTGCAAGGAGACTTTGACAGATT--AAAAAAGAAAAAAGAAAAAAGAAAAA 15928
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 Db 15927 AAAAAAAGAAAGCTTTCTTCTCAGACGCAATGAAACAAATTAATATGTTATGAA 15868
 QY 662 gcacttttaccacaggttcagtttttaccatttataagctgcgtgcgaaggttccagat 721
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 Db 15867 GCACCTTTTACCAACGCGTCACTTTTATACATTTTATACGTGCTCGAAAGGCTTCCAGAT 15808
 QY 722 gggagaccacatctctctgtgtctcagactcaccacaggtgcttttttcaaaaaag 781
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 Db 15807 GGGAGACCCATCTCTGTGCTGCTCAGACATTCATCACAGGCTGCTTTTATCAAAAAGG 15748
 QY 782 gaaacacatgccttcttctttaaanaagcttttttatttttccatagctcaat 841
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DEFINITION	AX013119			
ACCESSION	AX013119.1	GI:10040285		
VERSION				
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SOURCE				
ORGANISM	human.			
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 1630)			
AUTHORS	Schmitt,A., Specht,T., Dahl,E., Hinemann,B., Rosenthal,A. and			
	Pilarsky,C.			
TITLE	Human nucleic acid sequences of endometrium tumour tissue			
JOURNAL	Patent: WO 95/4461-A 59 28-Oct-1999;			
	SCHMITT A,MIN (DE); SPECHT T,THOMAS (DE); DAHL E,ENGAR (DE); HINEMANN			
	BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN			
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BASE COUNT	477 a 392 c 327 g 434 t			
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DEFINITION	Sequence	77 from Patent	WO9595858.		
ACCESSION	AX011681				
VERSION	AX011681.1	GI:9998205			
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SOURCE	human.				
ORGANISM	Homo sapiens				
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REFERENCE	1 (bases 1 to 1962)				
AUTHORS	Scmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pliarsky,C.				
TITLE	Human nucleic acid sequences obtained from pancreas tumor tissue				
JOURNAL	Patent: WO 9595858-A-77 04-NOV-1999;				
	SCMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GES FUER GENOMFORSCHUN (DE); PLIARSKY CHRISTIAN (DE)				
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Db 1179	ATGACCTTGCGTGACACATTTTCATTGTCAGATGTGTCCTCATTCCTAGCTTGGAGACTTCC	1238		
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ORGANISM	Homo sapiens
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AUTHORS	Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarsky,C.
TITLE	Human nucleic acid sequences of endometrium tumour tissue
JOURNAL	Patent: WO 9954461-A 541 28-OCT-1999;
	SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)
FEATURES	Location/Qualifiers
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BASE COUNT	547 a 440 c 431 g 544 t
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Best Local Similarity	99.7%;	Pred. No. 2e-178;		
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VERSION	AX011681.1	GI:998205	
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ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1962)		
AUTHORS	Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and		
	Pilarsky,C.		
	Human nucleic acid sequences obtained from pancreas tumor tissue		
	Patent: WO 955858-A 77 04-NOV-1999.		
JOURNAL	SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN		

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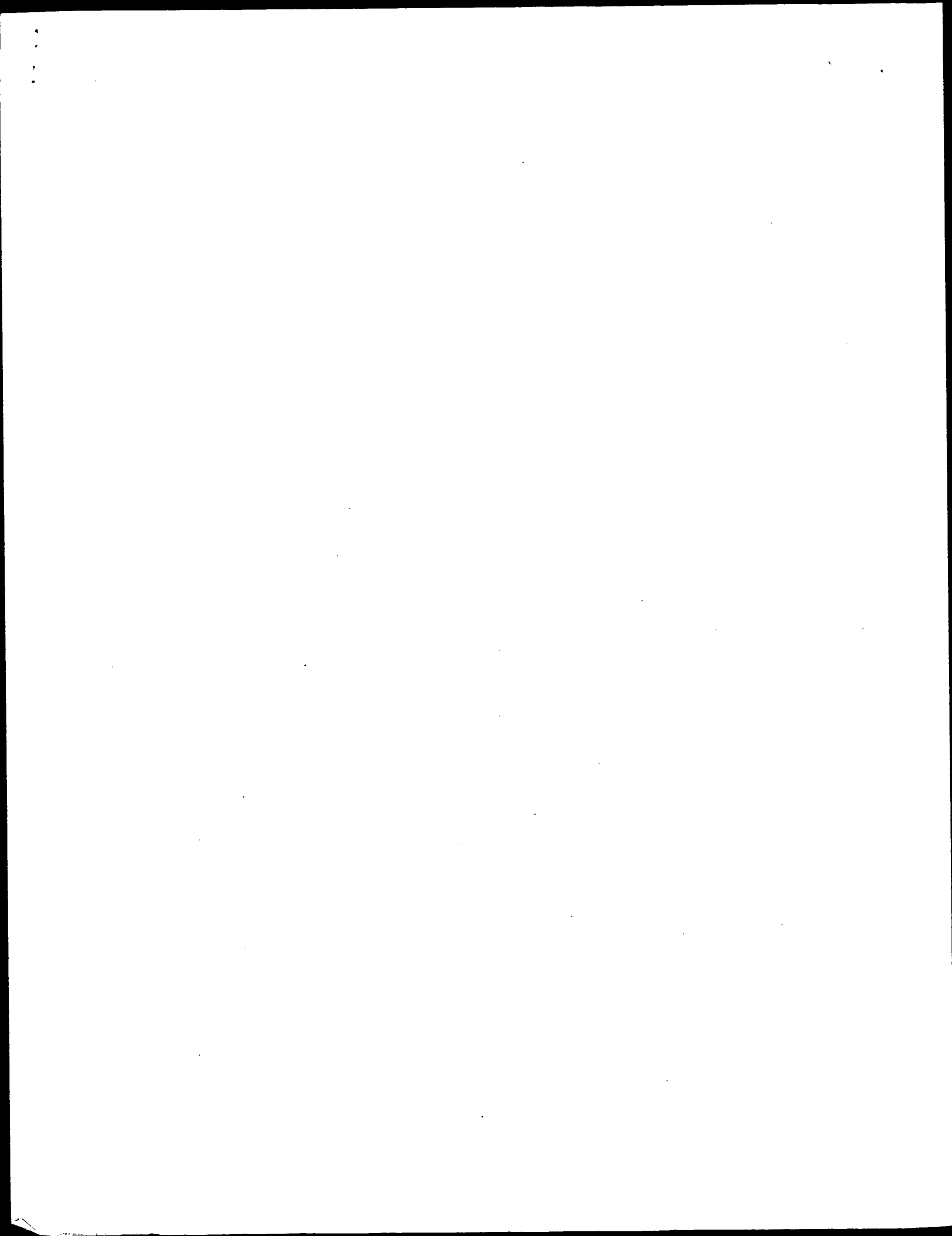
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB 1525 CAAGACTTGTGTTTCTTCCCTCACCCCAAGAAAGTGCACCT----- 1566
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DB 1681 GCCACACACTGCGCCCTCATTTAGAGCGCCGACACTGTATGCTGTG--TATCTGTATGTAAT 1739
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QY 1595 gtcaagaacatlaagcatgtacatgcatgcatatcttcttctaagtg-----gaag 1648
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DB 1740 GCTGAGACCCCTGAGTGTGCTGCAAGGATTTCTTCTTCTTGAAGTGAAGAAAGAAAG 1799
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QY 1649 taataaataatactgaaatgcaaaaaaataaaaaa 1685
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DB 1800 TAATAAATAATATTTGAAGTTAAAAAATAAAAAA 1836
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```

RESULT 14
 AF144754 1663 bp mRNA ROD 18-JUL-2001
 LOCUS AF144754
 DEFINITION Mus musculus B cell and monocyte-activating chemokine precursor
 (Bmac) mRNA, complete cds.

	Query Match:	42.1%	Score 709.6;	DB 10;	Length 1884;
	Best Local Similarity	70.9%;	Pred. No. 5,2e-127;		
	Matches 1233;	Conservative	0;	Mismatches 374;	Indels 129; Gaps 16;
QY	11	gcccagagcgccagcgcaagcgccacagacagcccttggatccacagcgccagcgccgga	70		
DB	187	GCCAAAGCGCAGCGCGGACCGGACGACAGAC-GGGAAGAGCACCATTGACGGGCGATTGGA	245		
QY	71	gccacagagagccggaagcgcgcccgggcagagagaagaacgagcagagcttgggtgctgc	130		
DB	246	GCGAGCGGAGCAGAGCAGAGAGAGGCGTGCTTGAAACCGAGAACCAAGCCGGCGGCGATC	305		
QY	131	tccggcgcgcgctctccagcgcgccagcgccctcccacatgcttcctgcctccagcgccgc	190		
DB	306	CCCCGGCGCGGACACGACAGGCGCGCGCCCTCTTGCTCTCCGTCGCC-CACCGCGCC	364		
QY	191	cctccggtgaagcattgaggtctctctggcgccgcgctcgtctcgtctcgtctggcgctgac	250		
DB	365	CGTCGGCCAGCATGAGGCTCTCGCGGCGCGGCTGCTCTGCTCTGCGGCTGTGC	424		
QY	251	accgcgctgtgaacggtgccaatgtcacatgtcctccggaagggagaccgaatccgtac	310		
DB	425	GTTTGGCGGCTTGGAGCGGCTCAAGTGTAAAGTCTTCAGGAAGGGGCCAAGATCCGTAC	484		
QY	311	agcgacgtgaagaagcttgtgaatgaagccaaatgccacgtccgagtgagagaatggtc	370		
DB	485	AGCGACGTGAAGACTGGAAATGAAGCCAAAGTACCACACTCGAGGAGAAATATGTT	544		
QY	371	atcatcacccaggaagatgcttccagatattacgaattcaggaagatgactctctacaccccaa	430		

[illegible]



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2002, 02:53:07 ; Search time 167.85 Seconds

(without alignments)
8606.452 Million cell updates/sec

Title: US-09-978-189-369

Perfect score: 1685
Sequence: 1 gcggagacagcgacgagcg.....aatgtataaaaaaaaaa 1685

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1685	100.0	1685	AAZ34205	Human PRO273 nucle
2	1685	100.0	1685	AAZ34205	Human PRO273 nucle
3	1685	100.0	1685	AAZ34205	Human PRO273 nucle
4	1640.4	97.4	1677	AAZ34205	Human PRO273 nucle
5	1447	85.9	1564	AAZ34205	Human PRO273 nucle
6	1358.4	80.6	1458	AAZ34205	Human PRO273 nucle
7	1092.2	64.8	1630	AAZ34205	Human PRO273 nucle
8	974.6	57.8	1662	AAZ34205	Human PRO273 nucle
9	872.6	51.8	1662	AAZ34205	Human PRO273 nucle
10	727.2	43.2	1663	AAZ34205	Human PRO273 nucle
11	727.2	43.2	1663	AAZ34205	Human PRO273 nucle

12	727.2	43.2	1663	22	AAZ34205	Human PRO273 nucle
13	720.6	42.8	1656	20	AAZ34205	Human PRO273 nucle
14	604	35.8	1372	20	AAZ34205	Human PRO273 nucle
15	580	34.4	599	22	AAZ34205	Human PRO273 nucle
16	558.6	33.2	726	21	AAZ34205	Human PRO273 nucle
17	550.4	32.7	584	22	AAZ34205	Human PRO273 nucle
18	448	26.6	764	21	AAZ34205	Human PRO273 nucle
19	448	26.6	764	22	AAZ34205	Human PRO273 nucle
20	448	26.6	764	22	AAZ34205	Human PRO273 nucle
21	435.6	25.9	661	18	AAZ34205	Human PRO273 nucle
22	426	25.3	766	21	AAZ34205	Human PRO273 nucle
23	426	25.3	766	22	AAZ34205	Human PRO273 nucle
24	352.8	20.9	1630	20	AAZ34205	Human PRO273 nucle
25	336	19.9	336	20	AAZ34205	Human PRO273 nucle
26	322.2	19.1	478	20	AAZ34205	Human PRO273 nucle
27	288	17.1	288	21	AAZ34205	Human PRO273 nucle
28	288	17.1	288	22	AAZ34205	Human PRO273 nucle
29	288	17.1	288	22	AAZ34205	Human PRO273 nucle
30	279.8	16.6	375	19	AAZ34205	Human PRO273 nucle
31	277.8	16.5	359	16	AAZ34205	Human PRO273 nucle
32	267.8	15.9	374	19	AAZ34205	Human PRO273 nucle
33	264	15.7	275	21	AAZ34205	Human PRO273 nucle
34	248.8	14.8	276	19	AAZ34205	Human PRO273 nucle
35	241.2	14.3	276	16	AAZ34205	Human PRO273 nucle
36	234	13.9	234	21	AAZ34205	Human PRO273 nucle
37	234	13.9	234	22	AAZ34205	Human PRO273 nucle
38	214.8	12.7	234	21	AAZ34205	Human PRO273 nucle
39	214.8	12.7	234	22	AAZ34205	Human PRO273 nucle
40	144.4	8.6	201	22	AAZ34205	Human PRO273 nucle
41	115.8	6.9	474	22	AAZ34205	Human PRO273 nucle
42	114.8	6.8	136	22	AAZ34205	Human PRO273 nucle
43	89.8	5.3	936	22	AAZ34205	Human PRO273 nucle
44	89.8	5.3	936	22	AAZ34205	Human PRO273 nucle
45	89.8	5.3	936	22	AAZ34205	Human PRO273 nucle

ALIGNMENTS

RESULT 1	AAZ34205	Standard: cDNA; 1685 BP.
AC	AAZ34205	
XX		
AC	AAZ34205	
XX		
DE	Human PRO273 nucleotide sequence.	
XX		
KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;	
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;	
XX	secreted protein; transmembrane protein; ss.	
OS	Homo sapiens.	
XX		
PN	W09946281-A2.	
XX		
PD	16-SEP-1999.	
XX		
PF	08-MAR-1999;	99WO-US05028.
XX		
PR	10-MAR-1998;	98US-0077450.
PR	11-MAR-1998;	98US-0077632.
PR	11-MAR-1998;	98US-0077649.
PR	11-MAR-1998;	98US-0077649.
PR	12-MAR-1998;	98US-0077791.
PR	13-MAR-1998;	98US-0078004.
PR	17-MAR-1998;	98US-0040220.
PR	20-MAR-1998;	98US-0078886.
PR	20-MAR-1998;	98US-0078910.
PR	20-MAR-1998;	98US-0078936.
PR	20-MAR-1998;	98US-0078939.
PR	25-MAR-1998;	98US-0079294.

PR	26-MAR-1998	98US-0079656
PR	27-MAR-1998	98US-0079663
PR	27-MAR-1998	98US-0079664
PR	27-MAR-1998	98US-0079669
PR	27-MAR-1998	98US-0079728
PR	27-MAR-1998	98US-0079766
PR	30-MAR-1998	98US-0079920
PR	30-MAR-1998	98US-0079923
PR	31-MAR-1998	98US-0080105
PR	31-MAR-1998	98US-0080107
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PR	31-MAR-1998	98US-0080194
PR	01-APR-1998	98US-0080327
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PR	08-APR-1998	98US-0081049
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PR	08-APR-1998	98US-0081071
PR	09-APR-1998	98US-0081195
PR	09-APR-1998	98US-0081203
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PR	15-APR-1998	98US-0081836
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PR	29-APR-1998	98US-0083392
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PR	07-MAY-1998	98US-0084598
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PR	15-MAY-1998	98US-0085700
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PR	18-MAY-1998	98US-0086023
PR	22-MAY-1998	98US-0086392
PR	22-MAY-1998	98US-0086430
PR	22-MAY-1998	98US-0086486
PR	28-MAY-1998	98US-0087096
PR	28-MAY-1998	98US-0087108

PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
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XX
XX (GETH) GENENTECH INC.
PI Wood WL, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
DR P-PSDB; AAY41739.
XX
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX
XX Claim 2; Fig 148; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA234338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
XX Sequence 1685 BP; 484 A; 435 C; 387 G; 379 T; 0 other;

Query Match	100.0%	Score 1685;	DB 20;	Length 1685;
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Db	1	ggcgagacaaagcgacagacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg	60	
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Db	61	cgcagacggagaccagacagacgacgacgacgacgacgacgacgacgacgacgacgacgacgacg	120	
OY	121	gggttgacgctcccgggcgccgcgcctccgacggcgacggcgccgcctcccatgtccctgtgcc	180	
Db	121	gggttgacgctcccgggcgccgcgcctccgacggcgacggcgccgcctcccatgtccctgtgcc	180	
OY	181	acgcgcgcgcgcctccggtcagacatgagagctcctgacgacgacgctctcctgtcgtct	240	
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OY	361	gaagatggtatcatcatcaaccaaccaagacgctgtccaggtaccagagtcacagagacgacgct	420	
Db	361	gaagatggtatcatcatcaaccaaccaagacgctgtccaggtaccagagtcacagagagcctgacg	420	
OY	421	ggaccccaaaccttcagagacccaagacgctctcatcaagttggtataaacgcttggaacgagaa	480	
Db	421	ggaccccaaaccttcagagacccaagacgctctcatcaagttggtataaacgcttggaacgagaa	480	
OY	481	ggcagaggtctacgaagaataggttgaaaaaaccttcgaagaggaaaaatccaaacacgcttg	540	
Db	481	ggcagaggtctacgaagaataggttgaaaaaaccttcgaagaggaaaaatccaaacacgcttg	540	
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QY      901 cagttgtctcattctcctagcttgggaagcttcgccttagaggtcctggcctcgac 960
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QY      1321 tgggcaatacagcgtcagcagacacattctgtgcaagggaaaccccttcaaaagatgt 1380
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Db      1321 tgggcaatacagcgtcagcagacacattctgtgcaagggaaaccccttcaaaagatgt 1380
QY      1381 ttccttccctcaccacaagaacatgctagtaagcaatataatttgcattcccat 1440
        |||||
Db      1381 ttccttccctcaccacaagaacatgctagtaagcaatataatttgcattcccat 1440
QY      1441 gtaattcttcaatgttaaacagtgagctcctcttgcgaagcttaagaatgacatgcgcc 1500
        |||||
Db      1441 gtaattcttcaatgttaaacagtgagctcctcttgcgaagcttaagaatgacatgcgcc 1500
QY      1501 tttccctctgataataacaccttaagaagccctcccaacacgtcccccgtatatagc 1560
        |||||
Db      1501 tttccctctgataataacaccttaagaagccctcccaacacgtcccccgtatatagc 1560
QY      1561 cgcattgtactcgtgtgtatatatgtatgtacatgtcagaaccccttagcatgtatga 1620
        |||||
Db      1561 cgcattgtactcgtgtgtatatatgtatgtacatgtcagaaccccttagcatgtatga 1620
QY      1621 ggtttcattattcttcttaagaatggaagtaataataatatttgaaatgtaaaaaaa 1680
        |||||

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Db      1621 ggttcataattcttcttaagatggaagtaataataatatttgaatgtaaaaaaa 1680
QY      1681 aaaaa 1685
        |||||
Db      1681 aaaaa 1685
QY      1681 aaaaa 1685

RESULT 2
AAC78551
ID      AAC78551 standard; cDNA; 1685 BP.
XX
AC      AAC78551;
XX
DT      08-FEB-2001 (first entry)
XX
DE      Human PR0273 (UNQ240) nucleotide sequence SEQ ID NO:369.
XX
KM      Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
XX      expressed sequence tag; detection: cancer; ss.
OS      Homo sapiens.
PN      WO200053756-A2.
XX
PD      14-SEP-2000.
XX
PF      18-FEB-2000; 2000WO-US04341.
XX
PR      08-MAR-1989; 99WO-US05028.
PR      12-MAR-1999; 99US-0123957.
PR      29-MAR-1999; 99US-0126773.
PR      21-APR-1999; 99US-0130232.
PR      28-APR-1999; 99US-0131445.
PR      14-MAY-1999; 99US-0134287.
PR      23-JUN-1989; 99US-0141037.
PR      26-JUL-1999; 99US-0145698.
PR      29-OCT-1999; 99US-0162506.
PR      30-NOV-1999; 99WO-US28313.
PR      02-DEC-1999; 99WO-US28551.
PR      02-DEC-1999; 99WO-US28565.
PR      16-DEC-1989; 99WO-US30095.
PR      30-DEC-1999; 99WO-US31243.
PR      30-DEC-1999; 99WO-US31274.
PR      05-JAN-2000; 2000WO-US00219.
PR      06-JAN-2000; 2000WO-US00277.
PR      06-JAN-2000; 2000WO-US00376.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL,
PI      Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlisen ME,
PI      Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
PI      Kijavlin JU, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
PI      Shelton DJ, Stewart TA, Tumas D, Williams PM, Wood WI;
XX      WPI: 2000-611443/58.
DR      P-PSDB; AAB44295.
XX
PT      Novel PRO polypeptides and polynucleotides used in detection methods,
XX      to target bioactive molecules to specific cells, and to modulate
XX      cellular activities -
XX
PS      Claim 2; Fig 148; 636pp; English.
XX
CC      AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC      sequence tag) sequences which encode secreted or transmembrane PRO
CC      polypeptides. The PRO polynucleotides and polypeptides have cytosolic
CC      activity. The polynucleotides and polypeptides can be used for detecting
CC      the presence of PRO polypeptides in samples, for linking bioactive
CC      molecules to cells and for modulating biological activities of cells,
CC      using the polypeptides for specific targeting. The polypeptide targeting
CC      can be used to kill the target cells, e.g. for the treatment of cancers.
CC      The polypeptide pairs provide specific targeting of bioactive molecules

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Db	721	tgggagagccatctctctctgtgctccagacttcatacagctgtcttttatacaaaaag	780
OY	781	ggaaactatgctctctctctttttaaataatgcttttctgtatctgtccatacgtcacta	840
Db	781	ggaaactatgctctctctcttttaaataatgcttttctgtatctgtccatacgtcacta	840
OY	841	tacatcgaagcttataagagcccgaggaagaacatgagctctgtgtggaacaactctcatg	900
Db	841	tacatcgaagcttataagagcccgaggaagaacatgagctctgtgtggaacaactctcatg	900
OY	901	cagtgctgtccattccctlaagcttgggaagcttcgcgtttagagtgccctgagcctcgac	960
Db	901	cagtgctgtccattccctlaagcttgggaagcttcgcgtttagagtgccctgagcctcgac	960
OY	961	agctgcgaacgagctctctctgtggtcttatgtgcgcgttcacacccctcagtgagctccacatg	1020
Db	961	agctgcgaacgagctctctctgtggtcttatgtgcgcgttcacacccctcagtgagctccacatg	1020
OY	1021	gcccctttagccgggcaagagagagcaggtctctcgcatacctgtctctcctcgaagactcaa	1080
Db	1021	gcccctttagccgggcaagagagagcaggtctctcgcatacctgtctctcctcgaagactcaa	1080
OY	1081	gcttggtgcccagaaaatgtgcttcaatccctccctctgttaattttaacacccctaga	1140
Db	1081	gcttggtgcccagaaaatgtgcttcaatccctccctctgttaattttaacacccctaga	1140
OY	1141	aacatctccaagatccctcgtatgtgcgagagaaaatgtctcttaagaagatgtggtgtct	1200
Db	1141	aacatctccaagatccctcgtatgtgcgagagaaaatgtctcttaagaagatgtggtgtct	1200
OY	1201	tcccaacctgtgagattctcttaaaaggtttcacaggttcaatatttaagtctcagaacatg	1260
Db	1201	tcccaacctgtgagattctcttaaaaggtttcacaggttcaatatttaagtctcagaacatg	1260
OY	1261	tgaagttcccaacacgtctcagcaaaaaacctttagagagaacttaaaaatataatgaataca	1320
Db	1261	tgaagttcccaacacgtctcagcaaaaaacctttagagagaacttaaaaatataatgaataca	1320
OY	1321	tgcgcataacagctcctcacacacatctctgttgcagaagggaanaaccttcoaaagcatgt	1380
Db	1321	tgcgcataacagctcctcacacacatctctgttgcagaagggaanaaccttcoaaagcatgt	1380
OY	1381	tctcttccctacacacaacagaaacatgacgtacttaagaacatataatttgaatcccat	1440
Db	1381	tctcttccctacacacaacagaaacatgacgtacttaagaacatataatttgaatcccat	1440
OY	1441	gtaatctctcaatgttaaacagctgcagctctcttctgcagaagctagaccatgcgcgc	1500
Db	1441	gtaatctctcaatgttaaacagctgcagctctcttctgcagaagctagaccatgcgcgc	1500
OY	1501	ttctctcgtacataatccctttagaagcgcctccacacacgtgcgcccgcagtatatgc	1560
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OY	1561	cgcattgacgcgtgttatatgcatagtcagtcagaacacatllaacatllagatgtatgc	1620
Db	1561	cgcattgacgcgtgttatatgcatagtcagtcagaacacatllagatgtatgtatgc	1620
OY	1621	ggtttcatatcttcttctaagaatggaagtataaataatataatttgaatgttaaaaaaaa	1680
Db	1621	ggtttcatatcttcttctaagaatggaagtataaataatataatttgaatgttaaaaaaaa	1680
OY	1681	aaaaa 1685	
Db	1681	aaaaa 1685	

RESULT	4
AA93905	
ID	AA93905 standard; CDNA; 1677 BP
XX	
XX	
AC	AA93905;
XX	

Df		23-MAY-2001	(first entry)
Xx			
De		Human cDNA encoding a membrane or secretory protein clone pSEC0212.	
Xx			
Xx		Human; secretory protein; membrane protein; vaccine; gene therapy;	
Kw		rheumatoid arthritis; diabetes; ss.	
Xx			
Oz	Homo sapiens.		
Pn	EPI067182-A2.		
Xx			
Pd	10-JAN-2001.		
Ff	07-JUL-2000; 2000EP-0114090.		
Xx			
PX	08-JUL-1999; 99JP-0194179,		
Pr	11-JAN-2000; 2000JP-0118775,		
PR	02-MAY-2000; 2000JP-0185766.		
Xx			
Pa	(HELI-) HELIX RES INST.		
Pi			
Dr	Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K; WPT: 2001-093989/11. P-PADB: AAB88478.		
Xx			
Pt	Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development - Claim 1; SEQ ID 323; 609pp + CD ROM; English.		
Ps			
Xx	This invention relates to nucleic acid sequences AAF93744 - AAF93916		
Cc	which encode human secretory or membrane proteins represented by		
Cc	AAB88317 - AAB88419. Included in the invention are primers		
Cc	AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the		
Cc	cDNA sequences of the invention. The invention also includes methods for		
Cc	the production of antibodies directed against the proteins, and cDNA		
Cc	sequences, which can be used in vaccines. The polynucleotide sequences		
Cc	can be used in gene therapy. The polynucleotide sequences and the		
Cc	proteins they encode may be used in the prevention, treatment and		
Cc	diagnosis of diseases associated with inappropriate secretory		
Cc	protein/membrane protein expression. The nucleic acids and complementary		
Cc	polymers may also be used as DNA probes in diagnostic assays		
Cc	(e.g. polymerase chain reactions (PCR) to detect and quantitate the		
Cc	presence of similar nucleic acid sequences in samples. They may also be		
Cc	used to study the expression and function of secretory proteins/membrane		
Cc	polypeptides and their role in metabolism. The polypeptides may be used		
Cc	as antigens in the production of antibodies against them and in assays to		
Cc	identify modulators (agonists and antagonists) of expression and		
Cc	activity. The antibodies and antagonists may also be used as therapeutic		
Cc	agents to down regulate expression and activity. The antibodies may also		
Cc	be used as diagnostic agents for detecting the presence of the		
Cc	polypeptides in samples (e.g. by enzyme linked immunosorbant assay		
Cc	(ELISA). Examples of diseases which may be treated include rheumatoid		
XX	arthritis and diabetes.		
SQ			
	Sequence 1677 BP; 463 A; 437 C; 395 G; 382 T; 0 other:		
Query Match	97.4%; Score 1640.4; DB 22; Length 1677;		
Best Local Similarity	99.4%; Pred. No. 0;		
Matches 1660; Conservative	0; Mismatches 1; Indels 9; Gaps 1		
Yy	1 gcgagacaaaggcgccgagcgccgcgaacggccaagaacccttggtgatcaacgagcg 60		
Db	gccggatcaccaaacgcgacgacgcgacgcgcgcacagacaagccccttggcatccaacgagc 76		
Yy	61 cgcaagccccgagccagaagaagcgccgaagcgccccgcgcgaagaagaagccgagcagact 120		
Db	77 ccgcagccgtagccagcagaagcgccgaagcgccccgggccaagaagaagccgagcagagt 136		
Yy	121 ggctggcgcgtcttcggcgccgacctccagaggccagcgccctcccatgtcccttgtccc 180		

Dh	137	gggtgagcgtctccgggcgcgcgtccgcagcgggccaagcgcctcccaatgtctcgtctccc	196
Qy	181	agcgcgcgcctccgcgtctcagcatgaagctctctcgtcgagcgcgcgtctcgtctcgtcgt	240
Dh	197	agcgcgcgcctccgcgtctcagcatgaagctctctcgtcgagcgcgcgtctcgtctcgtcgt	256
Qy	241	gggcgtctacacacgcgcgtgtgtggaaggggtcccaatgtcaatgtctccgcgaagggaccaa	300
Dh	257	gggcgtctacacacgcgcgtgtgtggaaggggtcccaatgtcaatgtctccgcgaagggaccaa	316
Qy	301	gaticgcctacacgcgcgtgtgtggaaggggtcccaatgtcaatgtctccgcgaagggaccaa	360
Dh	317	gaticgcctacacgcgcgtgtgtggaaggggtcccaatgtcaatgtctccgcgaagggaccaa	376
Qy	361	gaagatggttatcatcaaccaccaagaaggtgttccaaagtlaccogaaggttcaagaagcattgc	420
Dh	377	gaagatggttatcatcaaccaccaagaaggtgttccaaagtlaccogaaggttcaagaagcattgc	436
Qy	421	gaaccccaagcctgcgcgaagcaccaagcgtcttcaaatgtgtacaaagcctgtgaacgaaga	480
Dh	437	gaaccccaagcctgcgcgaagcaccaagcgtcttcaaatgtgtacaaagcctgtgaacgaaga	496
Qy	481	ggcgcaggtgtctacgaagaataggtgtgaaaaacccacgaagaagggaagaatcccaaccagttg	540
Dh	497	ggcgcaggtgtctacgaagaataggtgtgaaaaacccacgaagaagggaagaatcccaaccagttg	556
Qy	541	ggagacgtgtgtcaaaagacatttgtcagatttaaaaaaanaaaaaaanaaaaaaanaaaaaa	600
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Dh	608	aaaaaanaaaaaaagccttcttcttccacagcacaagaacaaatatatatatgttatga	667
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Qy	721	tggggagcccatctctctgtgtgtccagactcatcaagcgtgctttttatcatcaaaaag	780
Dh	728	tggggagcccatctctctgtgtgtccagactcatcaagcgtgctttttatcatcaaaaag	787
Qy	781	ggaaaacccatgctcttcccttttaaaaaatgtctttttgtattgttccatacgtcacta	840
Dh	788	ggaaaacccatgctcttcccttttaaaaaatgtctttttgtattgttccatacgtcacta	847
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Dh	848	tacatctagctttataaagcgcgcggagaaacaatgaagcttgggtgacacatttcattg	907
Qy	901	cagtggtgtcccatctcctagcttgggaagcttcgcgtttagaggtctctgcgcgcgcgcac	960
Dh	908	cagtggtgtcccatctcctagcttgggaagcttcgcgtttagaggtctctgcgcgcgcgcac	967
Qy	961	agctgcacacgggcctctcctggtcttatagcgcgttcaagcctcaagtgtgaactccacagt	1020
Dh	968	agctgcacacgggcctctcctggtcttatagcgcgttcaagcctcaagtgtgaactccacagt	1027
Qy	1021	ggccctgttagcgcgcgaacagagacagcagctctcgcagtcctgttctctcgaagaactcaa	1080
Dh	1028	ggccctgttagcgcgcgaacagagacagcagctctcgcagtcctgttctctcgaagaactcaa	1087
Qy	1081	gtttgtgtgtccagaaaaatgttgtctcaatcccccgtgttaattttacaacccctagga	1140
Dh	1088	gtttgtgtgtccagaaaaatgttgtctcaatcccccgtgttaattttacaacccctagga	1147
Qy	1141	aaactttccagaatccctgtatgtggagacaaatgtatccttaagaagaaggtgtgggctct	1200
Dh	1148	aaactttccagaatccctgtatgtggagacaaatgtatccttaagaagaaggtgtgggctct	1207
Qy	1201	tcccaacctagagatttcttgaagaagttccacagttcaatttaagtgttcgaagaagcgt	1260
Dh	1208	tcccaacctagagatttcttgaagaagttccacagttcaatttaagtgttcgaagaagcgt	1267

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Db	1268	tgaggctcccaacactgycacacaanaaccttaaggagaaaccttaaaatataatgataca	13277
QY	1321	tgcgcaatacacagctacagacacacacttcctgtgaacaggggaaaccttcaagaatgt	13808
Db	1328	tgcgcaatacacagctacagacacacacttcctgtgaacaggggaaaccttcaagaatgt	1387
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Db	1388	ttcttccctcaacaacacagacatgtagtactaaagaatataattgtatcccat	1447
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Db	1568	cgcatctgacgcgcgtgtatatagtcatgtacatgtgcagaaacattagcatgtaca	1627
QY	1621	gatttcacatctctcttcaagaatggaagtaaatataattttgaatgt	1670
Db	1628	gatttcacatctctcttcaagaatggaagtaaatataattttgaatgt	1677
RESULT	5		
ID	AAZ08962	standard; cDNA; 1564 BP.	
XX	AAZ08962;		
AC	AAZ08962;		
DT	20-OCT-1999	(first entry)	
XX	Human neckline-1 cDNA.		
DE	Human neckline-1 cDNA.		
XX	Chemoattractant cytokine; chemokine; CXc motif; conserved cysteine;		
KW	signal transduction modulation; angiogenesis inhibition;		
KW	chemotraction inhibition; cancer; inflammation; psoriasis;		
KW	post-transplantation organ rejection; ds.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	5'UTR	1..96	
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FT		97..396	
FT		/*tag= b	
FT	3'UTR	/product= "Human neckline-1"	
FT		397..1564	
FT		/*tag= c	
XX	WC0940104-A1.		
PN	12-AUG-1999.		
XX	12-AUG-1999.		
PD	10-FEB-1999;	99MO-US02943.	
XX	10-FEB-1999;		
PF	10-FEB-1998;	98US-0023664.	
XX	10-FEB-1998;		
PA	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.		
XX	Barnes TM, Mackay C;		
P1	WPI; 1999-494271/41.		
XX	P-SDB; AAY31612.		
DR	P-SDB; AAY31612.		
XX	Novel neokine polypeptides and polynucleotides used for regulating		
PT	and treating proliferative disorders and diseases		

	Matches 141B:	Conservative	0:	Mismatches	31:	Indels	26:	Gaps
QY	216	cgagcgcgcgtccctcgtctgctctgctgctgtacacccgcgcgtgtgagacgggtccaat	275					
Db	1	cgagcgcgcgtacccctcgtctgctctgctctgctctgctctacccgcgcgcgtgtgagcgtgtccaat	60					
QY	276	gcacagtgctcccggaagagagcccaaatccgcctacagcgagcggtgaagagcttgaatga	335					
Db	61	gcacagtgctcccggaagagagcccaaatctgcctacagcgagcggtgaagagcttgaatga	120					
QY	336	agctcaagatracccgcactcgcagagagaatgtgtatcatcacaccacaagacgtgtcca	395					
Db	121	agctcaagatracccgcactcgcagagagaatgtgtatcatcacaccacaagagcgtgtcca	180					
QY	396	ggtacccgaggtcaagagacgtctgctctcaccccaaggttcagagcaccaaagctttcata	455					
Db	181	ggtacccgaggtcaagagacgtctgctctcaccccaaggttcagagcaccaaagctttcata	240					
QY	456	agtggtacaaacgcttgaacagagaaagcgagaggtctctacgaagaatgaggtgaanaacctc	515					
Db	241	agtggtacaaacgcttgaacagagaaagcgagaggtctctacgaagaatgaggtgaanaacctc	300					
QY	516	agaaagggaaactccaaaccagttgtagagactctgtcacaagagactttgcagattaaaaa	575					
Db	301	tgaatggaaaactccagaccagcttgtagagactctgtcacaagagactttgcagatt-----	354					
QY	576	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaagcctttcttcttcacagggcata	635					
Db	355	-----taaaaaaaaaaaaaaaaaaagcctttcttcttcttcacagggcata	394					
QY	636	agagacaaatlatatattgtltatgaacacttttaaccaagctacagttttacattta	695					
Db	395	agagacaaatlatatattgtltatgaacacttttaaccaagctacagttttacattta	454					
QY	696	tagcttcgcgcgaaagaggtctccagatggagagcccatctcttcttgctccagactcat	755					
Db	455	tagcttcgcgcgaaagaggtctccagatgtagagcccatctctcttgctccagactcat	514					
QY	756	caacaggtccttttatcaaaaagggaaactcatgctcttccttctttaaanaatgctt	815					
Db	515	caacaggtccttttatcgaaaagggaaactcatgctcttccttctttaaanaatgctt	574					
QY	816	ttttgtattgtccatacgttcaactataactcgtgagcttataagcccgccggaggaacaa	875					
Db	575	ttttgtattgtccatacgttcaactataactcgtgagcttataagcccgccggaggaacaa	634					
QY	876	tgaacttggtagacaattcatctcagatgtgtgccatctcttagcttggtagagcttcg	935					
Db	635	tgaacttggtagacaattcatctcagatgtgttaactccatcttagcttggtagagcttcg	694					
QY	936	ctttagaggtctcgtgcgcttcgcgcacagctgcacagcgctctccttggttcatgccccg	995					
Db	695	ctttagaggtctcgtgcgcttcgcgcacagctgcacagcgctctccttggttcatgccccg	754					
QY	996	aagagctcaagtgtgactcacaagttgcccctgttaacggggaagagagagagctctc	1055					
Db	755	aagagctcaagttgtactcgcagttgcccctgttaacggggaagagagagagctctc	814					
QY	1056	tgcactcgtctctcgtaggaactcaagtttggttcgcagaaaatgtgtctcatctccccc	1115					
Db	815	tgcactcgtctctcgtaggaactcaagtttggttcgcagaaaatgtgtctcatctccccc	874					
QY	1116	tgtgttaatttttaacacacctaggaacaattccaagaactcgtgtgtagcgagacaatg	1175					
Db	875	tgtgttaatttttaacacacctaggaacaattccaagaactcgtgtgtagcgagacaatg	934					
QY	1176	atcccttaagaagtggtgtgctcttcccaaccttaagattcttgaagaaggttcaagtt	1235					
Db	935	atcccttaagaagtggtgtgctcttcccaaccttaagattcttgaagaaggttcaagtt	994					
QY	1236	caataatttaattgcttcagaagcatgtgaggttcccaaacactgtcagcaanaaccttga	1295					
Db	995	caataatttaattgcttcagaagcatgtgaggttcccaaacactgtcagcaanaaccttga	1054					

OY 1415 aaagcaatatttgatcccatgtaattcttaagttaacagtgagtcctctt 1474
 |||||||
 Db 1372 aaagcaatatttgatcccatgtaattcttaagttaacagtgagtcctctt 1431
 |||||||
 OY 1475 tcgaagcgaatgacatgacgagtcgagtcctctctgtacataacccttaagaagccccc 1534
 |||||||
 Db 1432 tcgaagcgaatgacatgacgagtcgagtcctctctgtacataacccttaagaagccccc 1491
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 OY 1535 tcacacactgccccccagatataatgcccagcttgactgctgtatataatgatacat 1594
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 OY 1655 aatataattgaatgta 1671
 |||||||
 Db 1612 aatataattgaatgta 1628
 |||||||

RESULT 8

AAZ52934
 ID AAZ52934 standard; cDNA; 1962 BP.

XX AC AAZ52934;

XX DT 14-MAR-2000 (first entry)

XX DE Human prostate tumor cDNA library derived EST fragment #77.

XX KM Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;

XX KW treatment; ds.

XX OS Homo sapiens.

XX PN DE19820190-A1.

XX PD 04-NOV-1999.

XX PF 28-APR-1998; 98DE-1020190.

XX PR 28-APR-1998; 98DE-1020190.

XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pflarsky C, Dahl E;

XX DR WPI; 1999-621386/54.

XX DR P-PSDB; AAY74043, AAY74044, AAY74045.

XX PS Claim 2; Page 245; 502pp; German.

XX CC This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52858-253014
 CC represent expressed sequence tag (EST) fragments derived from a human CC pancreatic tumor cDNA library and which encode the proteins represented CC in AAY7814-Y74252.

XX SQ Sequence 1962 BP; 547 A; 441 C; 431 G; 543 T; 0 other;

Query Match 57.8%; Score 974.6; DB 20; Length 1962;

Best Local Similarity 99.6%; Pred. No. 4e-192; Matches 977; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 575 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaagcctctcttcacagagcat 634
 |||||

Db 879 acaaatacaaaaaaaaaaaaaaaaaaaaaaaaagcctctcttcacagagcat 938
 |||||||
 OY 635 aagacccaattatattgttatgagacattttacaaggttcagttttaattt 694
 |||||||
 Db 939 aagacccaattatattgttatgagacattttacaaggttcagttttaattt 998
 |||||||
 OY 695 atagctgcgtgcgaaggttccagatggagagccatctctctgtgtccagactca 754
 |||||||
 Db 999 atagctgcgtgcgaaggttccagatggagagccatctctctgtgtccagactca 1058
 |||||||
 OY 755 tcadagctgcgttcttatacaaaagggaacatcagtccttctctttaaataatgct 814
 |||||||
 Db 1059 tcadagctgcgttcttatacaaaagggaacatcagtccttctctttaaataatgct 1118
 |||||||
 OY 815 tttttatattgtccataagctacatcagcttataagcggccgggaagaa 874
 |||||||
 Db 1119 tttttatattgtccataagctacatcagcttataagcggccgggaagaa 1178
 |||||||
 OY 875 atagagcttggtgacacattcattgcaagtgtgtgtccattcctagcttggaagcttcc 934
 |||||||
 Db 1179 atagagcttggtgacacattcattgcaagtgtgtgtccattcctagcttggaagcttcc 1238
 |||||||
 OY 935 gcttaagagctcctggtgagctcgtgacagctgcacaggtctcctggtctatggcggct 994
 |||||||
 Db 1239 gcttaagagctcctggtgagctcgtgacagctgcacaggtctcctggtctatggcggct 1298
 |||||||
 OY 995 caagcctcagctgagctcagctcagctgagctcagctgagctcagctgagctcagctcagct 1054
 |||||||
 Db 1299 caagcctcagctgagctcagctcagctgagctcagctgagctcagctgagctcagctcagct 1358
 |||||||
 OY 1055 ctgacatctgtctctcgaaggaactcaagtttggttgcgaagaatgttcttcatccccc 1114
 |||||||
 Db 1359 ctgacatctgtctctcgaaggaactcaagtttggttgcgaagaatgttcttcatccccc 1418
 |||||||
 OY 1115 ctggttaatttttaacaccccttagaagaacatttccaagatctgtgagcggagcaaat 1174
 |||||||
 Db 1419 ctggttaatttttaacaccccttagaagaacatttccaagatctgtgagcggagcaaat 1478
 |||||||
 OY 1175 gatccttaagaaggtgtggtgtcttcccaactgagagattctgaaaggttccagagt 1234
 |||||||
 Db 1479 gatccttaagaaggtgtggtgtcttcccaactgagagattctgaaaggttccagagt 1538
 |||||||
 OY 1235 tcaatatttaagtctcgaagacatgtgaggttcccaactgttcagaaaaacttagg 1294
 |||||||
 Db 1539 tcaatatttaagtctcgaagacatgtgaggttcccaactgttcagaaaaacttagg 1598
 |||||||
 OY 1295 agaaaacttaaaaatatatgatacatgacgaatcacagctacagacacattctgtt 1354
 |||||||
 Db 1599 agaaaacttaaaaatatatgatacatgacgaatcacagctacagacacattctgtt 1658
 |||||||
 OY 1355 gacaagggaacaccttcaagaagcatgttcttccctcaccacaagacatgagtaact 1414
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 Db 1659 gacaagggaacaccttcaagaagcatgttcttccctcaccacaagacatgagtaact 1718
 |||||||
 OY 1415 aaagcaatatttgatcccatgtaattcttaagttaacagtgagtcctctt 1474
 |||||||
 Db 1719 aaagcaatatttgatcccatgtaattcttaagttaacagtgagtcctctt 1778
 |||||||
 OY 1475 tcgaagcgaatgacatgacgagtcgagtcctctctgtacataacccttaagaagccccc 1534
 |||||||
 Db 1779 tcgaagcgaatgacatgacgagtcgagtcctctctgtacataacccttaagaagccccc 1838
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 OY 1535 tcacacactgccccccagta 1555
 |||||||
 Db 1839 tcacacactgccccccagta 1859
 |||||||

Query Match 97.8%; Score 974.6; DB 20; Length 1962;

Best Local Similarity 99.6%; Pred. No. 4e-192; Matches 977; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 9
 AAZ52934/C
 ID AAZ52934 standard; cDNA; 1962 BP.
 XX AC AAZ52934;
 XX

DJ		14-MAR-2000	(first entry)	
XX	DE	Human prostate tumor cDNA library derived EST frgiment #77.		
XX	KW	Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;		
XX	RW	treatment; ds.		
XX	OS	Homo sapiens.		
XX	PM	DEL9820190-AI.		
XX	PD	04-NOV-1999.		
XX	PF	28-APR-1998;	98DE-1020190.	
XX	PR	28-APR-1998;	98DE-1020190.	
XX	PA	(META-) METAGEN GES GENOMFORSCHUNG MBH.		
XX	PI	Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;		
DR		WPI; 1999-621386/54.		
CC	P-PDB:	AAV74043, AAV74044, AAV74045.		
PT	New human nucleic acid sequences from pancreatic tumors, and related			
PS	proteins -			
XX	Claim 2; Page 245; 502pp; German.			
CC	This invention describes novel polypeptides and their encoding nucleic			
CC	acids derived from human pancreatic tumor tissue which have cytosstatic			
CC	activity. The sequences are also useful in producing pharmaceutical			
CC	compositions for treatment of pancreatic tumors. AAZ52856-253014			
CC	represent expressed sequence tag (EST) fragments derived from a human			
CC	pancreatic tumor CDNA library and which encode the proteins represented			
CC	in AAY73814-Y74252.			
SQ	Sequence 1962 BP; 547 A; 441 C; 431 G; 543 T; 0 other;			
Query Match	51.8%; Score 872.6; DB 20; Length 1962;			
Best Local Similarity	97.9%; Pred. No. 4.6e-171;			
Matches 884; Conservative	0; Mismatches 19; Indels 0; Gaps			
OY	782 gaaaacctcgccttccttctaataaaatggcttttgatttgtcccaactcat 841			
Db	924 GAAGGCTTTTATTTTTTTTTTTTTTTTTTTTGTATTGGTCACACTCATAT 865			
OY	842 acatctgaaccttaataagccccggaggagaacaatgagcttggtygacacattcatgc 901			
Db	864 ACATCTGACCTTTAATAAGCGCCCGGAGAACAAATGAGCTTGAGCACATTTCATTGC 805			
OY	902 agtgtgtccatctccttagcttgggaagtcccgctttaaggtccctggsgctcggcata 961			
Db	804 AGTGTGTCACATTCTCTACTTGGGAAGCTGCCGTTAAGAAGTCTGGCGCCTCGGCACA 745			
OY	962 gctgcccaagggtcctcctcctggacttagcttagcgctlcaaacgctcaqtlgaactcacagtg 1021			
Db	744 GCTGCCACGGGCTCTCTCTGGGCTTAAGCGCGGCAAGGCTCAGTGTGACTCCACAGTGG 685			
OY	1022 cccttgtagccggccaagcagaagaagctctctctgcatctgtctctcyagaaactcaag 1081			
Db	684 CCCCTGTACC GGCGCAAGCAGAGCGAGCTCTCTGCACTGTTCTCTGAGGAACTCAAAG 625			
OY	1082 ttgtgtgaccagaanaatgctcattcccctccttggttaattttaacacacctagaaa 1141			
Db	624 TTGTGTTGCCAGAAAATGCTTCATTCOCCTGTTAATTTTACACACCTTAGGAA 565			
OY	1142 acattcccaagaatccctgtagtcgagacaatatgatccctlaaagaagtgtygggtcctt 1201			
Db	564 ACAATTCCAAGATCGTGTATGGCGAGACAAATGATCTTAAAGAAAGTGTGGGGCTTTC 505			
OY	1202 cccacacccagaagattctctyaaaggtlcaaaggtlcaaatattaatgatctccagaagatgt 1261			

Db	504	CCCACTGAGGATTCTGAAAGTTCAAGGTTCAATATTAAAGTTCAGAAGCAGT	445
Qy	1362	gaggtlccccaacactyltcagcaaaaaaccttagagagaaacttaaaatatatgaatacat	1321
Db	444	GAGGTTCCCAACACTGTCACCAAAAAACCTTAGAGAAAACTTAAAAATATATGAAATACAT	385
Qy	1332	gcgcaataacagagctacagacacacattctgttggaaaagaaaaccttaagaatgtt	1381
Db	384	GCGCAATACACAGCTACAGACACACACTTCGTGTGACAAAGGAAAACTTCAAGACATGTT	325
Qy	1382	tcttccctaccaccaacagaacatatcagttactaaagcaatatatttlygtlcccaatg	1441
Db	324	TCTTCCCTCACCACACACAGACATGACGACTAAAGCAATATTGTTGATTCGCCATG	265
Qy	1442	taattcttcaatgtltaaacagtgacgtctctcttggaaagcttaaatgacatgagccct	1501
Db	264	TAAATTTTCATGTAAACGATGCAAGTCCCTTTCCAAAGCTAAAGATGACCATGTGGCCCT	205
Qy	1502	ttctctcgtacatatacccttaagaagcccccctcacacactgccccccagtatatgcc	1561
Db	204	TTCCCTGTAATATATACCTTTAAAGAACGCCCTCCACACACTGCCCCCCCAATATATGCC	145
Qy	1562	gcattgctacgcgtgtgtlataatgctatgltacatgtcagaagaaccatltagcatgtgcag	1621
Db	144	GCATTGTACGTCGTGTATATGCTATGTATCATGTCCAGAAACCATATGATGTCATGCAG	85
Qy	1622	gttcaatactcttccaagatggaagtaataaataatatttggaaatgtaaaaaaaaaa	1681
Db	84	GTTTCATTTCTCTTCAAGATGGAAGATATAAAATATATTGGAAATGTAAAAAANA	25
Qy	1682	aaa 1684	
Db	24	AGA 22	

RESULT	ID
10	AAZ61823
standard; 1663 BP.	AAZ61823

DT	27-MAR-2000 (first entry)
XX	
DE	Full-length cDNA encoding muks1, SEQ ID NO:370

KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytosolic; neuroprotective; vulnerability; ss.

Mus sp.

PN W09955865-A1.

PD 04-NOV-1999.

PF 29-APR-1999; 99WO-NZ00051.

PR 29-APR-1998; 98US-0069726.

[illegible]

XX
XX

XX
XX

DR P-PSDB; AAY76115

Novel polynucleotides useful for the treatment of various conditions

[illegible]

RESULT 11

This sequence represents rat neokine-1 partial cDNA. The neokines are a novel family of chemottractant cytokines (chemokines) and are ligands for a previously identified putative G protein-coupled receptor termed RDC1 (also called the neokine receptor). The neokines are members of the non-ELR-CXC subfamily of chemokines characterised by the absence of an ELR motif and the presence of a CXC signature motif. The CXC motif encompasses 4 highly conserved cysteine residues, with the first two cysteines separated by one non-conserved amino acid residue; however, the neokines show some atypical features which distinguish them from previously characterised CXC chemokines e.g., the presence of approximately 5 residues between the third and fourth conserved cysteines. The neokines have a variety of functions, including modulation of signal transduction, inhibition of angiogenesis, regulation of inflammation and inhibition of chemotaxis. Neokines may therefore be useful in the treatment of various proliferative disorders or diseases: several types of cancer, inflammation, psoriasis, and immune rejection following skin graft and kidney transplantation. Neokines, their associated polynucleotides, homologues and antibodies can be used in screening for drugs or compounds which modulate their activity and therefore may be important for the development of new therapeutics.

Sequence 1372 BP; 359 A; 355 C; 332 G; 319 T; 7 other:

Query Match 35.8%; Score 604; DB 20; Length 1372;
Best Local Similarity 70.8%; Pred. No. 1.2e-115;
Matches 1021; Conservative 5; Mismatches 315; Indels 101; Gaps 13;

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OY 266 gggtccaatgcaagtcgtcccggaaggaagcccaatccgctacagcagctgaaag 325
DB 1 gggctcaagtgtatagttcccggaagggcccaatccgctacagcagctgaaag 60
OY 326 ctggaatgaagcacaagtaaccgcactggaaggaagatggtatcatcaccacaa 385
DB 61 ctggaatgaagcacaagtaaccgcaactggaaggaagatggtatcatcaccacaa 120
OY 386 agcgttcacagtaaccggaagtaaccgcaactggaaggaagatggtatcatcaccacaa 445
DB 121 agcgttcacagtaaccggaagtaaccgcaactggaaggaagatggtatcatcaccacaa 180
OY 446 cgcttcacagtaaccggaagtaaccgcaactggaaggaagatggtatcatcaccacaa 505
DB 181 cgcttcacagtaaccggaagtaaccgcaactggaaggaagatggtatcatcaccacaa 240
OY 506 gaaacacacaggaaggaagtaaccgcaactggaaggaagatggtatcatcaccacaa 565
DB 241 ggaacacacaggaaggaagtaaccgcaactggaaggaagatggtatcatcaccacaa 300
OY 566 gatttaaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaa 625
DB 301 gatt-----ataaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaa 327
OY 626 cacaagcacaagaacaaatataatgtatgaagcaacttttaaccaagtcagtt 685
DB 328 cacaagcacaagaacaaatataatgtatgaagcaacttttaaccaagtcagtt 384
OY 686 ttacatttaagctgctgcaaggaagctcagatggaagcaacttcctctgtgccc 745
DB 385 ttacatttaagctgctgcaaggaagctcagatggaagcaacttcctctgtgccc 444
OY 746 cagactcatcacaagctgtcttttatc-----aaaaaggggaataactatgccc 794
DB 445 cagactcatcacaagctgtcttttatc-----aaaaaggggaataactatgccc 504
OY 795 ttccctttaaaaaaagctttttgtattgtccatagcctacatatactgagcttt 854
DB 505 ttccctttaaaaaaagctttttgtattgtccatagcctacatatactgagcttt 564
OY 855 ataagcgcgcgggaaggaagcaatgagctgtggaacacattcatctgagctgtccat 914
DB 565 ataagcgcgcgggaaggaagcaatgagctgtggaacacattcatctgagctgtccat 624

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OY 915 tctcagcttggaagcttccgcttagagtgctcgtgagcctcggcagacagctgccaagggct 974
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OY 975 ctctcgtgctatgagccgctc-acagcctcagatgtagctcacaagctgagcctgtgagcgg 1033
DB 685 ctctcgtgctatgagccgctcagatgtagctcacaagctgagcctgtgagcgg 744
OY 1034 ggcagcagcagcagcagctcctctctgacatgcttctctgaggaactcaagttgttgccag 1093
DB 745 ggcagcagcagcagcagctcctctctgacatgcttctctgaggaactcaacttcccaag 804
OY 1094 aaaaatgctcattcccccctggttaatttttaacacaccttagaagaacatttccaaga 1153
DB 805 atgagcttcaagctcccccacacccacccacccacccacccacccacccacccacccaccc 852
OY 1154 tctctgtagtggaagcaaatatgctccttaagaagctgtg----gggtcttcccaactg 1210
DB 853 cccatcccaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 912
OY 1211 aggatcttctgaaagcttccacagcttcaatattatgctcagagaagctgtaggttccc 1270
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OY 1271 aacactgtcagcaaaaaccccttagaggaagaacattaaatatatgatalatgcycaat 1330
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OY 1331 aacagctacagacacacatctctgtgacaggaaggaaggaaggaaggaaggaaggaagga 1390
DB 1033 ccagcagagctacacacacatctctgtgacaggaaggaaggaaggaaggaaggaaggaagga 1089
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DB 1090 cgcgcccaagaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1128
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DB 1129 -----caacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1182
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DB 1183 acatatcccttaagaacacacacacacacacacacacacacacacacacacacacacacacac 1242
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DB 1243 cggcctgtg-aatctgtatgtaagtgctgagatgagtgagtgagtgagtgagtgagtgag 1301
OY 1630 tctcttcaagaatggaagtaa-----taaatatattgaaatgtaaaaaaaataaaaa 1683
DB 1302 tctcttcaagaatggaagtaaataataatatttgaakktvmcmamaaaaaaaataaaaa 1361
OY 1684 aa 1685
DB 1362 aa 1363

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RESULT 15

AAF94062 standard; DNA: 599 BP.

AAF94062;

23-MAY-2001 (first entry)

Primer specific for DNA encoding secretory/membrane protein SEQ ID 496.

Human; secretory protein; membrane protein; vaccine; gene therapy;

Rheumatoid arthritis; diabetes; PCR primer; ss.

Synthetic.

Wed Jan 30 09:48:19 2002

us-09-978-189-369.rng

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Db 311 agcgagctgaaagctggaatgaagccaaagtaaccacacgtcgaggaagatggtt 370
Qy 371 atcatcaccaccacaagaagctgtccaggtacccaggtacagagcactgcctcaccccaag 430
Db 371 atcgtcaccaccacaagaagctgtccaggtacccaggtacagagcactgcctcaccccaag 430
Qy 431 ctgcagagcaccacaagaagctgtccaggtacccaggtacagagcactgcctcaccccaag 490
Db 431 ctgcagagcaccacaagaagctgtccaggtacccaggtacagagcactgcctcaccccaag 490
Qy 491 tacgaagaatgggtgaaacactcagaaggaaggaaccccaagcttggaagactgtt 550
Db 491 tacgaagaatgggtgaaacactcagaaggaaggaaccccaagcttggaagactgtt 550
Qy 551 gcaagagcttgcagattaaataaaataaaataaaataaaataaaataaaataaa 610
Db 551 gcaagagcttgcagattaaataaaataaaataaaataaaataaaataaaataaa 610
Qy 611 aaagccttcttctcacaagcacaataatataatgttataagagcactttt 670
Db 577 aaagccttcttctcacaagcacaataatataatgttataagagcactttt 670
Qy 671 accaagcgtcagtttttaattttagctgtgctgaggaagcttcagatgagagacc 730
Db 635 acc-agggtcagtttttaattttagctgtgctgaggaagcttcagatgagagacc 693
Qy 731 atctctgtgtctcagacttcaatcagagctgtctttt 770
Db 694 agctcgctcgacacagacttcaatcagagctgtctttt 733

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RESULT 2

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US-08-825-556A-1
; Sequence 1, Application US/0825556A
; Patent No. 5910431

```

GENERAL INFORMATION:

```

; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Su, Jeffrey Y.
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Chemokine Alpha 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-2934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,556A
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,653
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0850001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..375
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 79..375
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 43..126
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 127..375
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 79..126
; US-08-825-556A-1

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Query Match 25.9%; Score 435.6; DB 2; Length 461;
Best Local Similarity 98.7%; Pred. No. 1.8e-89;
Matches 450; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

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Qy 130 ctccggcgccgcgtccagagcgccgcctcccatgttccctgtctccacgcgcgc 189
Db 6 CTCCGGCGCCGCGCTCCAGAGCGCGCCGCTCCCATGTCTCCCATGTCTCCAGCGCGC 65
Qy 190 cccctcggtaagatgagctctctgctgctgctgctgctgctgctgctgctgctg 249
Db 66 CCTCCGGCTCAGCATGAGGCTCTCCGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCT 125
Qy 250 caccgctgctgtgagcggttccaaatgcaagtgtctccggaaggaacccagctc 309
Db 126 CACCGCGCTGTGACAGCGGTCTCAATGCAAGTCTCCGGAAGGAGCAACCAAGATCG 185
Qy 310 cagcagctgaaagaagctggaatgaagccaagttaccgcaactgcagagaagaatg 369
Db 186 CAGCGAGCTGAAGAAGCTGGAATGAAGCCAAAGTACCCGACACTGCGAGGAGAAAGAT 245
Qy 370 tatatacaccacaagagcggttccaggttccaggttccaggttccaggttccaggtt 429
Db 246 TATCATCACCAAGAGCGGTCTCCAGGTACCGAGGTACGAGGTACGAGGTACGAGGT 305
Qy 430 gctcagagcaccagcgcttcacaaagtgttacaagcgcttgagacgagcgaggt 489
Db 306 GCTGAGAGCACCAAGCGCTTCATCAAGTGTACAGCGCTGGAAGCAAGCGAGGT 365
Qy 490 ctacgaagaataggttgaataaactcagaaggaaggaactccaacaggttgagact 549
Db 366 CTACGAAGAATAGGTGAAAAAAGCTCAGAAAGGAAAGTCCAAACAGTTGGAGACTTG 425
Qy 550 tg--caagagacttgcagattaaataaaataaaataaaataaaataaaataaa 583
Db 426 TGGCAAGGAACCTTGCAGATTAAATAAAATAAAATAAAATAAAATAAAATAAA 461

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RESULT 3

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US-09-188-930-38
; Sequence 38, Application US/09188930A
; Patent No. 6150502

```

GENERAL INFORMATION:

```

; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Mathew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348

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Query Match	13.9%	Score 234	DB 3	Length 234
Best Local Similarity	100.0%	Pred. No. 3	Re-44	
Matches 234	Conservative 0	Mismatches 0	Indels 0	Gaps 0
269	tcacatgcacagctctccgcgaagagcccaagcttcgcgtacacgcgcagctgtagaagactgc	328		
dbp	1	tcacatgcacagctctccgcgaagagcccaagcttcgcgtacacgcgcagctgtagaagactgc	60	

QY 329 gaatgaagccaaagtaccgcactgcgaggaagaatgttatcatcaccaccaagc 388
 Db 61 gaatgaagccaaagtaccgcactgcgaggaagaatgttatcaccaccaagc 120
 QY 389 gttccaggtaccgaggtcaggaagcactgtccaccaccaagctgcagagcaccagc 448
 Db 121 gttccaggtaccgaggtcaggaagcactgtccaccaccaagctgcagagcaccagc 180
 QY 449 ttcatcaagtgttacaacgccttgaaacgagagcgaggtctacgaagaatag 502
 Db 181 ttcatcaagtgttacaacgccttgaaacgagagcgaggtctacgaagaatag 234

RESULT 6
 US-09-188-930-271
 ; Sequence 271, Application US/09188930A
 ; Patent No. 6150502

GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James Greg
 TITLE OF INVENTION: Compositions Isolated From Skin Cells
 TITLE OF INVENTION: and Methods For Their Use
 FILE REFERENCE: 11000.1011c1
 CURRENT APPLICATION NUMBER: US/09/188.930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 271
 LENGTH: 234
 TYPE: DNA
 ORGANISM: Mouse
 US-09-188-930-271

Query Match 12.7%; Score 214.8; DB 3; Length 234;
 Best Local Similarity 94.9%; Pred. No. 8.1e-40;
 Matches 222; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 269 tccaatgaagtgtctccggaaggaaccagaatccgtctacagcgatgaagaagctg 328
 Db 1 tccaatgaagtgtctccggaaggaaccagaatccgtctacagcgatgaagaagctg 60
 QY 329 gaatgaagccaaagtaccgcactgcgaggaagaatgttatcatcaccaccaagc 388
 Db 61 gaatgaagccaaagtaccgcactgcgaggaagaatgttatcatcaccaccaagc 120
 QY 389 gttccaggtaccgaggtcaggaagcactgtccaccaccaagctgcagagcaccagc 448
 Db 121 gttccaggtaccgaggtcaggaagcactgtccaccaccaagctgcagagcaccagc 180
 QY 449 ttcatcaagtgttacaacgccttgaaacgagagcgaggtctacgaagaatag 502
 Db 181 ttcatcaagtgttacaacgccttgaaacgagagcgaggtctacgaagaatag 234

RESULT 7
 US-08-232-463-14/c
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA

COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: pTZgpt-Fls
 US-08-232-463-14

Query Match 4.2%; Score 70.6; DB 1; Length 7218;
 Best Local Similarity 8.9%; Pred. NO. 1e-06;
 Matches 40; Conservative 231; Mismatches 180; Indels 0; Gaps 0;
 QY 262 ggaaggtccaaatgaagtgtctccggaaggaaccagaatccgtctacagcgatga 321
 Db 1420 RRR 1361
 QY 322 gaagctgaaatgaagccaaagtaccgcactgcgaggaagaatgttatcatcacc 381
 Db 1360 RRR 1301
 QY 382 caagaagcgtccaggtaccgaggtcaggaagcactgtccaccaccaagctgcagac 441
 Db 1300 RRR 1241
 QY 442 caagcgtctacaagtgttacaacgccttgaaacgagagcgaggtctacgaagaat 501
 Db 1240 RRR 1181
 QY 502 ggtgaaacactcagaaggaagaactccaacaggttggaagcgtgtcagaagc 561
 Db 1180 RRR 1121
 QY 562 tgcagattaaaaaataaaaaaataaaaaaataaaaaaataaaaaaagccttct 621
 Db 1120 RRR 1061
 QY 622 ttctcagagcatalaagacacaaatataattgttatagaagcattttaccaggtca 681
 Db 1060 AGCTCCCTCGACCTGACCAAGCTCGGAATTATTCGTGTGAGGTATGCAACGAAG 1001
 QY 682 gtttaccatttaagctgtcggaag 712
 Db 1000 AAAAATAGTTATGATGCGCATGATGG 970

RESULT 8

```

; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match          3.3%; Score 55.2; DB 4; Length 289;
Best Local Similarity 13.7%; Pred.No. 0.00081;
Matches   36; Conservative 101; Mismatches 125; Indels    0; Gaps    0;

QY      340 aaagtaaccgcactgaggagaagatgttcatcacacccaaggcgctggccagtgta 399
       |:: :: |: : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db       26 arurururarcrrarururarcrrarurgrnnrnsrnrsnrnrsnrnrsnrnr 85

QY      400 ccgaagtcaggaagcactgacctgaccaccaagctgcagagcacaagcctcatcaagt 459
       : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      86 srnmrnsrmrnsrmrnsrmrnsrmrnsrmrnsrmrnsrmrnsrmrnsrmrnsrmrnr 145
```

RESULT 10
US-08-378-313-24
Sequence 24 Application US/08378313
Patent No. 4207861
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.

QY 552 ccaagagacttgcagattcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 611
Db 192 AA 133
QY 612 aa 613
Db 132 AA 131

RESULT 13

US-08-504-459-5
Sequence 5, Application US/08504459
Patent No. 5922563

GENERAL INFORMATION:

APPLICANT: Alderete, John F.
TITLE OF INVENTION: Adhesin Genes and Proteins Involved in
NUMBER OF INVENTIONS: Trichomonas Vaginalis Cytoadherence
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,459
FILING DATE: Concurrently herewith
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: USK:273/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-5000
TELEFAX: 512/474-7577

TELEX: N/A

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1804 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

FEATURE:

NAME/KEY: CDS

LOCATION: 14..1714

US-08-504-459-5

Query Match

Best Local Similarity 3.2%; Score 54.6; DB 2; Length 1804;
Matches 66; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 529 ccaaacagcttgagagactgctcaagagacttgcagattcaaaaaaaaaaaaaa 588
Db 1714 CTAAGCAGTTTAAACCTTTCAATGCTTTGAAAAA 1773
QY 589 aaaaaaaaaaaaaaaaaaaaaa 613
Db 1774 AAAAAAAAAAAAAAAAAAAAAA 1798

RESULT 14

US-09-248-335-25

Sequence 25, Application US/09248335

Patent No. 6096504
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 25
LENGTH: 1279
TYPE: DNA
ORGANISM: maize
US-09-248-335-25

Query Match- 3.2%; Score 53.4; DB 3; Length 1279;
Best Local Similarity 63.8%; Pred. No. 0.0038;
Matches 81; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 487 ggtctacgaagaataggtgtaaaacccacgaaggaacccaacagcttgagagac 546
Db 1138 gttcgtcgtgtaataaataaaccaccccgcttgcattgaattcaattcagtg 1197
QY 547 ttgtgcaagagacttgcagattcaaaaaaaaaaaaaaaaaaaaaa 606
Db 1198 tcgtgltgtaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1257
QY 607 aaaaaa 613
Db 1258 aaaaaa 1264

RESULT 15

US-08-484-105-17

Sequence 17, Application US/08484105

Patent No. 5589341

GENERAL INFORMATION:

APPLICANT: STILLMAN, Bruce
APPLICANT: BELL, Stephen P
APPLICANT: KOBAYASHI, Ryuji
APPLICANT: RINE, Jasper
APPLICANT: FOSS, Margit
APPLICANT: MCNALLY, Francis J
APPLICANT: LAURENSEN, Patricia
APPLICANT: HERSKOWITZ, Ira
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO

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OM nucleic - nucleic search, using sw model

Run on: January 30, 2002, 02:04:27 ; Search time 1469.3 Seconds
(without alignments)
12323.308 Million cell updates/sec

Title: US-09-978-189-369
Perfect score: 1685
Sequence: 1 gcggagacacagcgagcg.....aatgtaaaaaaaaaaaaa 1685

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estfun: *
2: em_esthm: *
3: em_estin: *
4: em_estom: *
5: em_estpl: *
6: em_estda: *
7: em_estro: *
8: em_estov: *
9: em_hic: *
10: gD_estl: *
11: gD_estl2: *
12: gD_hic: *
13: gD_gss: *
14: em_gss_fun: *
15: em_gss_hum: *
16: em_gss_inv: *
17: em_gss_pin: *
18: em_gss_pro: *
19: em_gss_rtd: *
20: em_gss_vrt: *
21: em_gss_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846.4	50.2	976	11	BG678414
2	835	49.6	858	11	BG696197
3	805.4	47.8	829	11	BG67521
4	800	47.5	844	11	BG679254
5	797.4	47.3	845	10	AL543855
6	759.2	45.1	794	11	BG677005
7	754.4	44.8	860	11	BG679890
8	714.4	42.4	817	11	BG400382
9	696.6	41.3	745	10	AL570175
10	681.6	40.5	756	11	BG681049
11	653	38.8	1668	12	AK004615
12	638.6	37.9	770	11	BG699665

13	624.6	37.1	858	11	BG572071	BG572071	602592543
14	618.6	36.7	707	11	BG619277	BG619277	602619402
15	612.5	36.4	629	11	AV733062	AV733062	AV733062
16	611.8	36.3	925	11	BG622267	BG622267	602646929
17	610	36.2	614	10	AV651293	AV651293	AV651293
18	595	35.3	728	11	BG700277	BG700277	602679901
19	590.4	35.0	646	11	BG399290	BG399290	602441093
20	588	34.9	715	11	BG700847	BG700847	602681753
21	584.5	34.7	965	11	BG708310	BG708310	602672241
22	568	33.7	619	10	AV650090	AV650090	AV650090
23	567	33.6	579	10	AA534943	AA534943	AA534943
24	564.2	33.5	610	10	BE714963	BE714963	BE714963
25	568	33.4	1094	10	BE615443	BE615443	601280927
26	550.2	32.7	647	11	N45415	N45415	N45415
27	550	32.6	776	11	BG699615	BG699615	602679345
28	541.6	32.1	623	11	AA059409	AA059409	AA059409
29	539.4	32.0	542	10	BE615852	BE615852	601279715
30	532	31.6	532	10	AA827992	AA827992	601279715
31	531	31.5	531	10	AM007386	AM007386	AM007386
32	525.8	31.2	550	10	AT817325	AT817325	AT817325
33	524.4	31.1	526	10	AM001498	AM001498	AM001498
34	524.4	31.1	932	11	BG698977	BG698977	602678601
35	523	31.0	551	10	AT076787	AT076787	602678601
36	520.4	30.9	530	10	BE720078	BE720078	602678601
37	507	30.1	507	11	BE726908	BE726908	602678601
38	502	29.8	502	10	AT1126732	AT1126732	602678601
39	499	29.6	499	10	AA426536	AA426536	602678601
40	499	29.6	499	10	AA426536	AA426536	602678601
41	493	29.3	509	11	W73085	W73085	W73085
42	492.8	29.2	533	10	AM383219	AM383219	602678601
43	489.8	29.1	517	11	W73190	W73190	W73190
44	489	29.0	489	10	AM572310	AM572310	602678601
45	488.2	29.0	515	11	BF349654	BF349654	602678601

ALIGNMENTS

RESULT 1
LOCUS BG678414
DEFINITION 602625062F1 NCT_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750214 5',
mRNA sequence.
ACCESSION BG678414
VERSION BG678414.1 GI:13909811
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 976)
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM10604 row: k column: 15
High quality sequence stop: 864.
Location/Qualifiers
1. 976
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4750214"
/clone_lib="NCT_CGAP_Skn4"
/tissue_type="Squamous cell carcinoma"
/lab_host="DH10B (TI phage-resistant)"

FEATURES

source

/note="Organ: skin; Vector: PCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 263 a 234 c 201 g 278 t
ORIGIN

Query Match 50.2%; Score 846.4; DB 11; Length 976;
Best Local Similarity 97.7%; Pred. No. 1.3e-110;
Matches 891; Conservative 0; Mismatches 16; Indels 5; Gaps 3;

Qy 616 ctctctctcagcagcacaagaacaattatattgttataagcacttttaccac 675
Db 1 CTTCTTCTCAGAGCATTAAGACAAATATATATTGATGAAAGCATTTTACCAC 60
Qy 676 cgttgaattttacatttataagctgctggaaggttcacagtggaaccatctc 735
Db 61 CGGTAGTTTTTACATTTTATAGCTGCGTGAAGGCTTCAGATGAGAACCATCTC 120
Qy 736 tcttgctcagactcacaagctgcttttatacaaaaggggaaacatagcct 795
Db 121 TCTTGTGCTCAGACTTATCAGAGCTGCTTTTATCAAAAAGGGAACATGCT 180
Qy 796 ttccttttaaaatgctttttgtatttgcataagtcatacatctgagcttta 855
Db 181 TTCTCTTTTAAAAAATGCTTTTATTTGTCATGCTCATATACATCTGAGCTT 240
Qy 856 taagcgcggcggaggaacaatagcttgtagacacattcaltgcaagtgttgcacat 915
Db 241 TAAAGGCCCGGAGAGACATGAGCTTGATGAGACATTTATTCAGTGTGCTCAT 300
Qy 916 cctagcttgggaagcttcctgcttagaagtcctgctgctgagcagctgcacggctc 975
Db 301 CCTAGCTTGGGAAGCTTCCGCTTAAAGGCTCCTGCGCCGCGCACAGCTGCCACG 360
Qy 976 tcttggtctatggcgcgagcagcagctgagtgagctcacaagtgccctgtagcgg 1035
Db 361 TCTGTGGCTTATGCGCGGACAGCTCAGTGTGCTCAGCTCAGCTGAGCTGAGCT 420
Qy 1036 caagcggagcagctcctctgcatctgtctctgaggaactcaagttgtgtccagaa 1095
Db 421 CAAGCAGGAGCAAGCTCTCTGCACTCTGCTGAGCAATCAAGTTGTTGCCAGAA 480
Qy 1096 aaatgtgtcattcccccctggttaatttttaacacacctgagaaacattcccaagtc 1155
Db 481 AAATGTGCTTCAATTCCTCCCTGGTTAATTTTACACACCTTGAAGAACTTTTCAAGATC 540
Qy 1156 ctgtgtagcaggaacaatgagcttaagaagtgtaggtgcttcccaactgagat 1215
Db 541 CTGTGATGGGAGACAAATGATCTTTAAAGAAAGTGTGGGCTTTCCCAACCTGAGAT 600
Qy 1216 ttctgaaggttcacaggttcaatatttaagtctcagaagcagtgtaggttcccaac 1275
Db 601 TTCTGAAGGTTACAGGTTCAATATTATGCTTCAGAGCATGAGGTTCCCAACAC 660
Qy 1276 tgtcagcaaaaccttaagaagaacttaataataataataatagcgaataaacaac 1335
Db 661 TGTACACAAAAACCTTAGGGAAGAACTTAAAAATATATATACAGCCCAATACACAGC 720
Qy 1336 taagaacacacattcgtttgacaagggaacacctcaagcagtgcttcttcctaca 1395
Db 721 TACAGACACACATTTGTTGACAAAGGAAACCTTCAAAAGCATGTTTCTTCCCTCA -CA 779
Qy 1396 caacagaacatgacgtactaagaacataattgtattcccatatgtaattcttcaagt 1455
Db 780 TAAACAGAAATGACAGTAAAGCAATATATGATTTCCCATATATTTCTTCAACGT 839
Qy 1456 taacaagtg---cagtcctcttcg--aaagctaaagtacacagcccttctcctcgt 1511
Db 840 TTACACACAGGAGTCCTCTTTCGAAAGCTAAGATGACATGCGCCCTTCTCTGTGA 899
Qy 1512 catataacctta 1523

Db 900 CATATTACCTTA 911

RESULT 2
Bg696197 858 bp mRNA EST 07-MAY-2001
LOCUS 602659321F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4802404 5',
DEFINITION mRNA sequence.

ACCESSION Bg696197
VERSION Bg696197.1 GI:13961096
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 858)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0696 row: j column: 05
High quality sequence stop: 852.
Location/Qualifiers

FEATURES
source
1. 858
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4802404"
/clone_1lb="NCI_CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: PCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 228 a 211 c 176 g 243 t
ORIGIN

Query Match 49.6%; Score 835; DB 11; Length 858;
Best Local Similarity 99.8%; Pred. No. 5.6e-109;
Matches 857; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 662 gcaattttacacagcagcttattacatttataagctgctggaaggttccagat 721
Db 1 GCACCTTTTACCAACGGTCACATTTTACATTTTATGCTGCTGCGAAGGCTTCCAGAT 60
Qy 722 gggagaccatctctctgtgctccagactcacaagctgctttttcaaaagg 781
Db 722 GGGAGACCCATCTCTGTGCTCAGACCTTCAACAGAGCTGCTTTTATCAAAAAGG 120
Qy 782 gaaactatgcttctctcttttaaaatgctttttgtatattgttcacagctact 841
Db 121 GAAAACTATGCTCTTCTCTTTTAAAAAATGCTTTTGTATTTGTCATACATGCTAT 180
Qy 842 acatcagcttataaagcgcgggaggaacaatgagctgtgtgacaacattcattgc 901
Db 181 ACATGTGAGCTTTTAAAGCGCCGCGGAGAGCAATGAGCTTGTGGACACATTTCAATTC 240
Qy 902 agtgtgtcattctctcagcttggaagcttcgcttagaaggtctcggcctggagaca 961
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Qy 962 gctgcacagggctcccggggcttataggcggacacagcctcaagtgtgactccacagtg 1021
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[illegible]

mRNA sequence.
 accession BG679254
 version BG679254.1 GI:13910651
 keywords EST.
 source human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 844)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs.fda.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM10609 row: j column: 09
 High quality sequence stop: 839.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."
 BASE COUNT 226 a 212 c 172 g 233 t 1 others
 ORIGIN
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 Best local Similarity 98.7%; Pred. No. 4,9e-104;
 Matches 838; Conservative 0; Mismatches 6; Indels 5; Gaps 3;
 QY 711 ggcctcagatggagaccatctctctgtgtcagactatcacagcgtctt 770
 DB 1 GGCCTCAGATGGAGACCCTCTCTGTGTCTCCAGACTTACAGGCTCTTT 60
 QY 771 atcaaaagggaactcagctctctctttaaataatgcttttgtatltgtcca 830
 DB 61 ATCAAAAGGGAACCTCATGCTTCCCTTTTAAATAATGCTTTTGTATTGTCA 120
 QY 831 tacgtacatacatctagcttataagcgccggaggaataatgagctgtgtgaca 890
 DB 121 TACGTCACTATCATCTGACCTTTATAAGCGCCGGAGGAGCAATGAGCTGTGTGACA 180
 QY 891 catttaacatggtgtgtcccatctctagcttgggaagcttcgcgtatgagctgtgc 950
 DB 181 CATTTCATTCAGTGTGCTCCATCTCTAGCTTGGGAAGCTTCCGCTTAGAGTCTCTGGC 240
 QY 951 gctctgacacagctgacacagcggtctctctgtgtgtatgtgcggatcaagcctagtgtga 1010
 DB 241 GCTGCGACAGCTGCCACGGGCTCTCTGGCTTATGCGCGGTACAGCCTCAGTGTGA 300
 QY 1011 ctccacagtgccctctgtacccgggacagagacagcggtctctctgtcatctgtctc 1070
 DB 301 CTCACAGTGGCCCTTACCGGGCAAGCAGGAGGAGGTCTCTGCAATCTGTCTCTG 360
 QY 1071 aggaaccacagttgtgttcagaaataatgtctcatctcccccgtgttaatttaca 1130
 DB 361 AGGAACCAAGTTGTGTTCAGAAATAATGTCTCATTTCCCCCTGCTTAATTTTACA 420
 QY 1131 cacctaggaacatttccaagatcctgtatgtgcagagacaatgatccttaagaaggt 1190

DB 421 CACCTAGGAACATTTCCAGATCCTGTGATGGCGAGACAATATGATCCTTAAGAAGGT 480
 QY 1191 gtgggtcttcccaaccgagagattctgaaaggttcaaggttcaatattatgtct 1250
 DB 481 GTGGGCTCTTCCCAACCTGAGATTCTGAAAGGTTTCACAGTTTAAATTTATGCTT 540
 QY 1251 cagaagcatgtgaggttcccaaccgagcagcaaaactttagagaaacttaaaata 1310
 DB 541 CAGAGCATGTGAGGTTCCCAACAGCTGACGAAACCTTGGAGCAAACTTAATAAATA 600
 QY 1311 tatgaatatacgtcgaatacacagctacagacaacatctgttgcagggaaaccc 1370
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 QY 1371 caaagatgttcttccctccaccacaagacagcagctacagtaagaataatattgt 1430
 DB 661 CAAAGCATGTGTTCTTCTCCACANACAGACATGCACTACTTAAGCAATATATTGT 720
 QY 1431 gatcccatgtaattcttcaatgttaaacagtgacgtccctcttgcagaagctaaatga 1490
 DB 721 GATCCCATGTATTTCTTCAATGTTAACAGTGCAGATCCTCTTGGAAAGCTAAGATGA 780
 QY 1491 ccatgagcccttccctctgtacatacaccttaagaagccctccacaactgcccc 1550
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 QY 1551 cagatattg 1559
 DB 836 CAGTATATG 844
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 DEFINITION AL543855 LTL_NFL006.PL2 Homo sapiens cDNA clone CSD1005Y122 5
 prime, mRNA sequence.
 ACCESSION AL543855
 VERSION AL543855.1 GI:12876334
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 845)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
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 /organism="Homo sapiens"
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 /clone="CSD1005Y122"
 /clone_lib="LTL_NFL006.PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 231 a 204 c 166 g 227 t 17 others
 ORIGIN
 Query Match 47.3%; Score 797.4; DB 10; Length 845;

Best Local Similarity 97.3%; Pred. No. 1,1e-103; Matches 822; Conservative 17; Mismatches 3; Indels 3; Gaps 3;									
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Db	1	GATGGAGASCATCTCTTGTGTCACAGCTTATACAGGCTTTTATCAAAA	60						
Qy	779	gggggaaactatgccttctctttaaataatgcttctgtattgtccatgcgtac	838						
Db	61	GGGGAACATCATGCTTCTTTTAAATAAGCTTTTGTATTTGTTCATACGTCAC	120						
Qy	839	tatcatctgagacttataagcgccgggagagaaatagcttggtgagacat-ttca	897						
Db	121	TATCATCTGAGCTTTATAGGCGCCGGGAGAACAAAGACTTGTGACACATATTCA	180						
Qy	898	ttgcagtggtgtccatctctagcttggagacttgcgcttagaggtccggcccg	957						
Db	181	TTCAGTGTGCTCATCTAGCTTGGAGACTTCCGCTTAGAGGTCTGCGCCCTCG	240						
Qy	958	cacagctgcacagggctct-cctgggttatggtcggttcaagcctcaat-gtga	1015						
Db	241	CACAGCTGCACGGGCTTACCTGGCTTATGGCGGTACAGCTCAGTAGTACTCA	300						
Qy	1016	cagtgccctgtagccgggagagagagagagagagagagagagagagagagag	1075						
Db	301	CAGTGGCCCTGTAGCCGGGACAGCAGCAGCTCTCTGCACTGCTCTCTGAGAA	360						
Qy	1076	ctcaagtttggttccagaaaatgtgtcttcatctcccccgtgttatttcaacac	1135						
Db	361	CTCAGTGTGCTTCYARAAAATGMRATAATTCMCMCTGGTTAATTTTACACACC	420						
Qy	1136	taagaaacttccagagactgtgagtgagagagagagagagagagagagagag	1195						
Db	421	TAGGAACATTTMCAAGATCTGTGATGAGARCAATATGATCTTAAAGAGTGGG	480						
Qy	1196	gtcttcccaactgagagatttctgaaggttcaaggttcaatattatgtcttcaag	1255						
Db	481	GTCTTCCCACTGAGAGATTTTGAAAGGTTCACAGTTCATATTATGCTTCARNA	540						
Qy	1256	gcataaggttcccaactgtcagcaaaaacccttagagagaaactttaaataatga	1315						
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Qy	1316	atacatgcaaatatcacagctatagagacacattctgttgaagagagaaacttcaag	1375						
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Db	661	CATGTTCCTTCCCTCACCAACAGACATGCACTAATAAGCAATATATTGTGATTC	720						
Qy	1436	cccatgaattcttcaatgttaagagtgcaatcctcttgaagctaaagtaccatg	1495						
Db	721	CCCATGTAATTTCTCAATGTTAAAMAGTCAAGTCCCTTTCGAACCTTAAGATGACCATG	780						
Qy	1496	cgcccttctctgtacataataccttaagaaagccccctcacacacatgccccca	1555						
Db	781	CGCCCTTCTCTGTACATATACCTTAAAGACGCCCCCTCACACAMATGCCCCCACTA	840						
Qy	1556	tatgc 1560							
Db	841	TATGC 845							

RESULT 6
LOCUS BG677005 794 bp mRNA
DEFINITION 602623644E1 NC1_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748603 5',
ACCESSION BG677005
VERSION BG677005.1 GI:13908402
KEYWORDS EST.
SOURCE human.

ORGANISM	Homo sapiens									
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 794)									
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .									
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)									
JOURNAL	Unpublished (1999)									
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@remail.nih.gov Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM10600 row: h column: 12 High quality sequence stop: 787. Location/Qualifiers 1..794 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4748603" /clone_lib="NCI_CGAP_Skn4" /tissue_type="squamous cell carcinoma" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: skin; Vector: pCMV-SPOK6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library." 210 a 191 c 167 g 226 t									
BASE COUNT										
ORIGIN										
Query Match	45.1%; Score 759.2; DB 11; Length 794;									
Best Local Similarity	98.9%; Pred. No. 2.9e-98;									
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Qy	714	tctcagaatggagaccatctcttctgtcctcagacttcaacagctgtctttatc	773							
Db	61	TTCAGATGGAGACCCATCTCTGTGTGTCACAGCTTACACAGCTGCTTTTATC	120							
Qy	774	aaaaaggggaaactatgcttcttctttaaataatgcttcttgaattgtccatc	833							
Db	121	AAAAGGGGAAACCTCATGCTTCTTTTAAATAATGCTTTTGTATTTGTCCATAC	180							
Qy	834	gtcatalatctgagcttataagcgccgggagagaaatgagcttggtgagacat	893							
Db	181	GTCACTATCATCTGAGCTTTATTAAGCGCCCGGAGAGAACATGAGCTTGTGACAT	240							
Qy	894	ttcatgtcagtggttctcattctcagcttggagagcttcgcttagagagtcctgc	953							
Db	241	TTCATTCAGTGTGCTCATCTAGCTTGGGAAAGCTTCCCTTAGAGAGCTGCGCC	300							
Qy	954	tccgacagctgcacagggctctcctggcttataggccggtacagcctcagtgatc	1013							
Db	301	TCCGACAGCTGCGACGGGCTCTCTGAGCTTATGCGGTACAGCTCAAGTGTGATC	360							
Qy	1014	cacagtgccctgtagccgggagagagagagagagagagagagagagagagag	1073							
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Qy	1074	aactgaagtttggttcgagaaatgtgtcattctcccccgtgttaatttcaaac	1133							
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Qy	1134	cctagaagaaacttccaagatctgtgtatggagagaaatgagatccttaagaaggtg	1193							
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QY 1194 gggcttcccaacgtgaggttcttgaaagtccaggttcaattatattgcttcag 1253
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 QY 1434 tccc 1437
 Db 780 TCCC 783
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 BG679890 860 bp mRNA EST 01-MAY-2001
 LOCUS 602626393F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:451327 5',
 DEFINITION mRNA sequence.
 ACCESSION BG679890
 VERSION BG679890.1 GI:13911287
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 860)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bbs-rtmail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM10607 row: 1 column: 24
 High quality sequence stop: 858.
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 /tissue.type="squamous cell carcinoma"
 /lab.host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; NotI:
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP library."
 BASE COUNT 231 a 205 c 180 g 244 t
 ORIGIN
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 Best local similarity 97.3%; Pred. No. 1.3e-97;
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 Db 1 GACACAATTATATTGTATGAGCACTTTTACCACGGTCAGTTTACATTTAT 60

QY 697 agctgcgtcgaaggcttccagatgaggaccctctctctgtgtccagacttca 756
 Db 61 AGCTGCTGCGAAAGGCTTCCAGATGGAGACCCATCTCTTGTGCTCCAGACTTCA 120
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 QY 817 tct-gatttgcatacgtcactatacactcgtacttaaaagcccgagggaagaa 875
 Db 181 TTTGATTTTGTCCATACGTCACTATACATCTGAGCTTTATAGCGCCCGGAGGAGACA 240
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 Db 361 ACAGCTCAGTGTGACATCCACAGTGGCCCTGTAGCCGGGACAGCAGAGTCTTC 420
 QY 1056 tgcattcgtctctcgaagactcaagtttgttgcagaaaa--atgtcttcaatccc 1113
 Db 421 TGCACTCTCTCTGAGAGACTCAAGTTGGTGGCCAGCAACATGCTTCATTCCTCC 480
 QY 1114 cctgttaatttttaacacacccctaggaacatttccaaagtctctgtatgtg 1173
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 QY 1174 tgaactctaa--agaaggtgtggtggtcttcccaacctggaattcttcaa-agg 1231
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 QY 1352 gttagcaaa-gggaagacattcaagcagatgttcttccctccacccaagaaagatgag 1410
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 Db 780 TACTAAAGCAGCTATATTGGTGATTCCTCCCATGTATTTCAATGTTAACAGTCACTCC 839
 QY 1471 tcttctgaagacta 1484
 Db 840 TCTTTGAGAGCTA 853
 RESULT 8
 BG400382 817 bp mRNA EST 12-MAR-2001
 LOCUS 602464401F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:459250 5',
 DEFINITION mRNA sequence.
 ACCESSION BG400382
 VERSION BG400382.1 GI:13293830
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 817)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

1
2
3
4
5
6

380 TTTGAGATT-----AAAATAAAGCCCTTT 605

QY 244 gctgtacacgcgcgtgtgacggtcccaatgcaagtgctcccggaaggacccaagat 303
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 QY 304 ccgcctacacgcgcgtgtgaaagctgtgaaatgaaagcccaagtaaccgcactgcgagagaa 363
 Db 304 CCCTTACACGCGCGTGTGAAAGCTGTGAAATGAAAGCAAGTACCCGCACTCGAGAGCAA 363
 QY 364 gatgtatcatcaccacccaagagcgtgtccaggtaccaggtgagagagcctccgca 423
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 QY 424 ccccaagctgcagagacccaagcgtctcatcaagtgtgtacaagcctgtgaaagagcg 483
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 QY 484 caggtgtcagagagataggtgtgaaaccccaagagagagaaactccaaccagttgga 543
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 QY 544 gactgtgcaagagactgtgcagattaaacacacacacacacacacacacacacacac 603
 Db 544 GACTGTGCAAGACTTGTGAGATT-----ACCAACACAC 579
 QY 604 aaaaaaaagccttcttctcagagcacaagacacacacacacacacacacacacacac 660
 Db 580 CCAAAAAAGCGCTTCTTCTCAGCGGCTTACAGACCAAAATTTACTATATGAGTATGA 639
 QY 661 agcacttttcaacagcgtcagttttacat--ctttagtggtgagcagagcttcca 718
 Db 640 AGCACTTTTTCACAAAGCTTCTTCTCAGCGGCTTACAGACCAAAATTTACTATATGAGTATGA 639
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RESULT 13
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 858)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cga@rsf.remail.nih.gov
 Tissue Procurement: CLOUTIER Laboratories, Inc.
 cDNA Library Preparation: CLOUTIER Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L10M1573 row: f column: 11
 High quality sequence stop: 635.
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 site_1: SfiI (ggccgctcgcc); site_2: SfiI (ggcattatggcc

BASE COUNT

296 a 196 c 176 g 190 t

ORIGIN

Query Match 37.1%; Score 624.6; DB 11; Length 858;
 Best Local Similarity 98.5%; Pred. No. 2.8e-79;
 Matches 641; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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 QY 1096 aaatgtgttcattcccccctggttaatttacaacacctaggaacacattccaagatc 1155
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 QY 1156 ctgtgatggcgagaaatgtatcctttaaagaaggtgtgggctcttccaacctgagat 1215
 Db 121 CTGTATGTGGCGAGAACAAATGATCCTTAAAGAGGTGTGGGCTCTTCCCAACCTGAGGAT 180
 QY 1216 ttctgaagagctcacaagcttaataattatgtctcagaagcagatgtgagttcccaacc 1275
 Db 181 TTCTGAAGGTTTCAAGGTTCAATATTTAATGCTTCAAGAACATGTGAGTTCCCAACAC 240
 QY 1276 ttttggcaaaaaacctttaggagaaacttaaaatataatgatacatgacacacacagc 1335
 Db 241 TGTGACAAAAAACCCTTAGAGAAAACTTAAATAATATGATACATGCCAATACACACAC 300
 QY 1336 tacgagacacacattctgttgcagaaggaacacacacacacacacacacacacacac 1395
 Db 301 TACGAGACACACATTCTGTGTACAAAGGAAAACTTTCAAAACATGTTCTTCCCTACCA 360
 QY 1396 caatagaacatgcagtaactaaagcaatataattgtgattcccatgtaattccaatgt 1455
 Db 361 CAAGAAGAACATGACGTACTTAAGCAATATATTGTGATTCCTCATGTAATTTCTCAATG 420
 QY 1456 taacagtgacagctctcttgcagaagtaagatgacacagcgccttctctgtacata 1515
 Db 421 TAAACAGTGCAGTCTCTTTCGAAAGCTAAGATGACCATGCGCCCTTCTCTGTACATA 480
 QY 1516 taaccttaagaagccccctccacaacacacacacacacacacacacacacacacacac 1575
 Db 481 TACCTTAAGAGAGCCCGCCCGCACACACTGCCCCCAAGTATAGCGCGCATTTGACTGCTG 540
 QY 1576 tgttatatgctatgtatcatgctcagaagaacatgacatgcatgca-gtttcatattct 1634
 Db 541 TGTATATGCTATGATATGTCAGAAACCATTAAGCATTTGCATGAGGGTGTATATTTCT 600
 QY 1635 tctagaatggaagtaataataatattgaaatgtgaaacacacacacacacacacacac 1685
 Db 601 TCTTAGATGGAAGTACTTAATAATATTTTGAATGTGACACAGAGAGAA 651

RESULT 14

LOCUS BG619277 707 bp mRNA EST 18-APR-2001
 DEFINITION 602619402F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4733112 5',
 mRNA sequence.
 ACCESSION BG619277
 VERSION BG619277.1 GI:13670648
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OY	1276	tgctcgaaaacaccttgaggagaaaactttaaaatataigaatacacygcacacacagc	1335
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OY	1336	tacagacacacatctctgttacaaggaaaccttaagaactgttcttctccaccca	1395
Db	301	tacagacacacatctctgttacaaggaaaccttataaagcagtttcttccctcacca	360
OY	1396	caacagaacatgacgtactcaagaacatataattgttgatcccccahtaatcttcaatgt	1455
Db	361	caacagaacacatgcagtgactaaacacatataattgttgatcccccahtaatcttcaatgt	420
OY	1456	taaacatgacgctctcttccgaaagcctaagatgacatgagcccttccctgttacata	1515
Db	421	taaacatgacgctctcttccgaaagcctaagatgacacatgacgcccccttccctgttacata	480
OY	1516	taccttaagaagccccctccacacacatgacgccccccagatatactgcgattgtactgtg	1575
Db	481	taccttaagaagccccctccacacacatgacgccccccagatatactgcgattgtactgtg	540
OY	1576	tgttatatgctatgtacatgctcagaaaacatatagcattgacatgacggtttcatactctt	1635
Db	541	tgttatatgctatgctcattcatctcagaaaacattagcattgacatgacggtttataattcttt	600
OY	1636	ctaagatcgaagaataataataatct 1662	
Db	601	ctaagatcgttaagtaattatatttggtt 627	

Search completed: January 30, 2002, 03:23:44
Job time: 4757 sec

